

\$%^STN;HighlightOn= ***;HighlightOff=*** ;

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NEWS	2	"Ask CAS" for self-help around the clock
NEWS	3 SEP 09	CA/Caplus records now contain indexing from 1907 to the present
NEWS	4 DEC 08	INPADOC: Legal Status data reloaded
NEWS	5 SEP 29	DISSABS now available on STN
NEWS	6 OCT 10	PCTFULL: Two new display fields added
NEWS	7 OCT 21	BIOSIS file reloaded and enhanced
NEWS	8 OCT 28	BIOSIS file segment of TOXCENTER reloaded and enhanced
NEWS	9 NOV 24	MSDS-CCOHS file reloaded
NEWS	10 DEC 08	CABA reloaded with left truncation
NEWS	11 DEC 08	IMS file names changed
NEWS	12 DEC 09	Experimental property data collected by CAS now available in REGISTRY
NEWS	13 DEC 09	STN Entry Date available for display in REGISTRY and CA/Caplus
NEWS	14 DEC 17	DGENE: Two new display fields added
NEWS	15 DEC 18	BIOTECHNO no longer updated
NEWS	16 DEC 19	CROPU no longer updated; subscriber discount no longer available
NEWS	17 DEC 22	Additional INPI reactions and pre-1907 documents added to CAS databases
NEWS	18 DEC 22	IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
NEWS	19 DEC 22	ABI-INFORM now available on STN
NEWS	20 JAN 27	Source of Registration (SR) information in REGISTRY updated and searchable
NEWS	21 JAN 27	A new search aid, the Company Name Thesaurus, available in CA/Caplus
NEWS	22 FEB 05	German (DE) application and patent publication number format changes
NEWS EXPRESS	DECEMBER 28 CURRENT WINDOWS VERSION IS V7.00, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003	
NEWS HOURS	STN Operating Hours Plus Help Desk Availability	
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 10:42:23 ON 01 MAR 2004

=> index biosci

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION

FULL ESTIMATED COST

0.21	0.21
------	------

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 10:42:36 ON 01 MAR 2004

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0* with SET DETAIL OFF.

=> s (transfection (w) agent) (P) (peptide or polypeptide)

- 0* FILE ADISNEWS
- 0* FILE BIOCOMMERCE
- 10 FILE BIOSIS
- 16* FILE BIOTECHABS
- 16* FILE BIOTECHDS
- 4* FILE BIOTECHNO
- 3 FILE CANCERLIT
- 9 FILE CAPLUS
- 2* FILE CEABA-VTB
- 1* FILE CIN
- 1 FILE DISSABS
- 2 FILE DDFU
- 77 FILE DGENE

25 FILES SEARCHED...

- 2 FILE DRUGU
- 3 FILE EMBASE
- 4* FILE ESBIODASE
- 1* FILE FEDRIP
- 0* FILE FOMAD
- 0* FILE FOREGE
- 0* FILE FROSTI
- 0* FILE FSTA
- 14 FILE IFIPAT
- 0* FILE KOSMET
- 2 FILE LIFESCI
- 0* FILE MEDICNF
- 4 FILE MEDLINE
- 0* FILE NTIS

0* FILE NUTRACEUT
0* FILE PHARMAML
57 FILES SEARCHED...
4 FILE SCISEARCH
5 FILE TOXCENTER
21 FILE USPATFULL
14 FILE WPIDS
14 FILE WPINDEX

23 FILES HAVE ONE OR MORE ANSWERS, 68 FILES SEARCHED IN STNINDEX

L1 QUE (TRANSFECTION (W) AGENT) (P) (PEPTIDE OR POLYPEPTIDE)

=> file hits

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.71	1.92

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FILE 'FEDRIP' ENTERED AT 10:44:03 ON 01 MAR 2004

```
=> s l1
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
      5 FILES SEARCHED...
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'AGENT) (P) '
L2      197 L1
```

```
=> s (hydrophobic (w) domain) and aromatic
L3      2082 (HYDROPHOBIC (W) DOMAIN) AND AROMATIC
```

```
=> s (hydrophilic (w) domain) and basic
L4      327 (HYDROPHILIC (W) DOMAIN) AND BASIC
```

```
=> s l2 and l3 and l4
L5      1 L2 AND L3 AND L4
```

```
=> d l5 bib ab
```

```
L5      ANSWER 1 OF 1  USPATFULL on STN
```

AN 2003:173877 USPATFULL
 TI Peptide-mediated transfection agents and methods of use
 IN Divita, Gilles, Paris, FRANCE
 Morris, May C., Paris, FRANCE
 Mery, Jean, Paris, FRANCE
 Heitz, Frederic, Paris, FRANCE
 Fernandez, Joseph, Carlsbad, CA, UNITED STATES
 Archdeacon, John, Carlsbad, CA, UNITED STATES
 Hondorp, Kyle, Carlsbad, CA, UNITED STATES
 PI US 2003119725 A1 20030626
 AI US 2001-915914 A1 20010726 (9)
 PRAI US 2000-221932P 20000731 (60)
 DT Utility
 FS APPLICATION
 LREP DAVID R PRESTON & ASSOCIATES, 12625 HIGH BLUFF DRIVE, SUITE 205, SAN
 DIEGO, CA, 92130
 CLMN Number of Claims: 75
 ECL Exemplary Claim: 1
 DRWN 26 Drawing Page(s)
 LN.CNT 4044
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 AB Peptides that are useful as transfection agents are described. The
 peptides can facilitate the efficient cellular internalization of a
 broad range and size of compounds that when non-covalently complexed
 therewith are efficiently internalized into a cell. Advantages include
 but are not limited to excellent transfection efficiency, relatively low
 toxicity, internalization by a broad host cell spectrum, and the
 simplicity and cost-effectiveness that arise from not having to
 covalently complex the peptide with a specific molecule to be delivered.
 Applications include but are not limited to the delivery of diagnostics
 and therapeutics, as well as drug discovery, gene discovery, and the
 analysis and/or manipulation of other cellular and molecular biological
 functions. claims are made for transfection agents, compositions of
 matter, including pharmaceutical compositions, reagent kits, methods of
 delivery, and methods of identification of additional peptides for
 performing and/or including in the same.

=> log h

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	59.45	61.37

SESSION WILL BE HELD FOR 60 MINUTES
 STN INTERNATIONAL SESSION SUSPENDED AT 10:46:33 ON 01 MAR 2004

OM protein - protein search, using sw model
Run on: March 1, 2004, 13:31:13 ; Search time 53.0189 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWETWETWESQPKKRV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	100.0	20	5	Abb77672 Peptide t
2	120	92.3	21	5	Abb77693 Peptide t
3	120	92.3	21	5	Abb77693 Peptide t
4	120	92.3	21	5	Abb77671 Peptide t
5	120	92.3	21	7	Abb68484 Peptide s
6	120	92.3	21	7	Adc22460 Protein-d
7	116	89.2	20	5	Abb77673 Peptide t
8	110	84.6	20	5	Abb77694 Peptide t
9	109	83.8	19	5	Abb10106 Peptide t

10	108	83.1	21	5	Abb77674
11	95	73.1	19	5	Abb77699
12	93	71.5	19	5	Abb77676
13	90	69.2	12	5	Abb77689
14	90	69.2	12	5	Abp56174 Cell-targ
15	90	69.2	26	5	Abp56200 Chimeric
16	87	66.9	19	5	Abb77675 Peptide t
17	82	63.1	21	5	Abb77678
18	79	60.8	11	5	Abb77695
19	73	56.2	17	5	Abb77667
20	69	53.1	9	5	Abb77692
21	69	53.1	18	5	Abb77666
22	69	53.1	19	5	Abb77668
23	69	53.1	19	5	Abb77698
24	69	53.1	19	5	Abb77669
25	69	53.1	20	5	Abb77679
26	64	49.2	19	5	Abb77670
27	61.5	47.3	430	5	Abp47755 Protein #
28	61.5	47.3	560	4	Abb84201 Amino aci
29	61.5	47.3	560	6	Aag79973 P2C/C38S/
30	61.5	47.3	560	7	Adc29023 HIV-1 RT
31	61.5	47.3	562	6	Abp44741 Plasmid p
32	61.5	47.3	582	6	Abp44740 Plasmid p
33	61.5	47.3	585	6	Abp44743 Plasmid 7
34	61.5	47.3	724	5	AAU11869
35	61.5	47.3	739	5	AAU11874
36	61.5	47.3	760	1	AAp94510 Sequence
37	61.5	47.3	850	4	AAE04792 Human imm
38	61.5	47.3	850	4	AAE04791 Human imm
39	61.5	47.3	850	5	Adc71141 Codon opt
40	61.5	47.3	850	5	Adc71143 Inactivat
41	61.5	47.3	850	6	Abu63365 HIV-1 W11
42	61.5	47.3	850	6	Abu63366 HIV-1 Ina
43	61.5	47.3	875	4	AAE04794 Human tPA
44	61.5	47.3	875	4	AAE04793 Human tPA
45	61.5	47.3	875	5	Adc71145 Codon opt

ALIGNMENTS

RESULT 1
ABB77672
ID ABB77672 standard; peptide; 20 AA.
XX
AC ABB77672;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.1.
XX
RW Intracellular delivery; transfection agent; cancer; infectious disease;
peptide vector.
XX
OS Synthetic.
XX
PN W0200210201-A2.

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```

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWETWTEWSQPKRRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database : PIR_78:*
           1: pir1.*
           2: pir2.*
           3: pir3.*
           4: pir4.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	61.5	47.3	559	2	B47175	reverse transcriptase
2	61.5	47.3	1003	1	GNWLV	HIV-1 retropepsin
3	61.5	47.3	1003	1	B44001	HIV-1 retropepsin
4	61.5	47.3	1003	2	T03440	pol. polyprotein -
5	61.5	47.3	1012	1	GNWVL	HIV-1 retropepsin
6	61.5	47.3	1015	1	GNWH3	HIV-1 retropepsin
7	56.5	43.5	902	2	T01668	pol polyprotein -
8	56.5	43.5	1002	2	S54378	pol polyprotein -
9	56.5	43.5	1451	2	B86286	F911.15 protein -
10	56.5	43.5	1469	2	H96622	probable ABC trans
11	55.5	42.7	1002	1	GNLND	HIV-1 retropepsin
12	53	40.8	374	2	AG0937	hypothetical prote
13	53	40.8	689	2	F83902	beta-galactosidase

14 52 40.0 413 2 C91229
15 52 40.0 413 2 B6076
16 52 40.0 418 2 S40824
17 50.5 38.8 559 2 A47175
18 50.5 38.8 912 2 S33980
19 50.5 38.8 1003 1 GNVWAZ
20 50 38.5 368 2 T15492
21 50 38.5 581 2 T38501
22 50 38.5 686 2 A40104
23 50 38.5 818 2 F87327
24 49 37.7 390 1 B49070
25 49 37.7 455 2 T48973
26 49 37.7 849 2 D82510
27 49 37.7 864 2 A49070
28 49 37.7 902 2 S49931
29 48.5 37.3 562 2 S25725
30 48.5 37.3 770 2 S75042
31 48.5 37.3 894 2 T27007
32 48 36.9 45 2 C82233
33 48 36.9 197 2 S59397
34 48 36.9 468 2 A45268
35 48 36.9 586 1 TVPBP
36 48 36.9 656 2 S55262
37 48 36.9 1019 2 T11580
38 48 36.9 1054 1 GNLJG5
39 48 36.9 1056 1 GNLJG3
40 47.5 36.5 239 2 C84505
41 47.5 36.5 315 2 S76267
42 47.5 36.5 544 2 B84264
43 47.5 36.5 692 2 H70362
44 47.5 36.5 1027 1 GNLJ51
45 47 36.2 463 2 T48116

Search completed: March 1, 2004, 19:34:31
Job time : 14.2041 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 8.11321 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-8
Perfect score: 130
Sequence: 1 KETWTWTWTEWSQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		DB		Description	
No.	Score	Match	Length	ID			
1	61.5	47.3	1003	1	POL_HV1H2	P04585	human immun
2	61.5	47.3	1003	1	POL_HV1I2	P35963	human immun
3	61.5	47.3	1007	1	POL_HV1JR	P20875	human immun
4	61.5	47.3	1015	1	POL_HV1B1	P03366	human immun
5	61.5	47.3	1015	1	POL_HV1B5	P04587	human immun
6	61.5	47.3	1015	1	POL_HV1BR	P03367	human immun
7	61.5	47.3	1015	1	POL_HV1PV	P03368	human immun
8	60.5	46.5	1006	1	POL_HV1MN	P05961	human immun
9	56.5	43.5	1002	1	POL_HV1EL	P04589	human immun
10	56.5	43.5	1002	1	POL_HV1MA	P04588	human immun
11	56.5	43.5	1002	1	POL_HV1RH	P05959	human immun
12	56.5	43.5	1002	1	POL_HV1Z2	P12499	human immun
13	56.5	43.5	1003	1	POL_HV1N5	P12497	human immun
14	56.5	43.5	1003	1	POL_HV1OY	P20892	human immun
15	55.5	42.7	1002	1	POL_HV1ND	P18802	human immun
16	52	40.0	413	1	Y1HS_ECOLI	P32140	escherichia
17	50.5	38.8	1002	1	POL_HV1U4	P24740	human immun

18 50.5 38.8 1003 1 POL_HV1A2
19 49 37.7 229 1 UNG_CHICV
20 49 37.7 902 1 SYGL_YEAST
21 48 36.9 41 1 LPX_VIPRA
22 48 36.9 468 1 IL9R_MOUSE
23 48 36.9 586 1 TALA_POVBO
24 48 36.9 656 1 UVE1_NEUCR
25 48 36.9 880 1 SYL_XANAC
26 48 36.9 1019 1 POL_SIVS4
27 48 36.9 1022 1 POL_SIVSP
28 48 36.9 1054 1 POL_SIVMK
29 48 36.9 1056 1 POL_SIVM1
30 48 36.9 2298 1 YGF2_LOTJA
31 47.5 36.5 315 1 SECF_SXNY3
32 47.5 36.5 692 1 PHSG_AQUAE
33 47.5 36.5 1027 1 POL_SIVCZ
34 47 36.2 964 1 RPO_MGMV
35 46.5 35.8 794 1 YEL4_YEAST
36 46.5 35.8 1058 1 POL_HV2D2
37 46 35.4 78 1 YOO5_BPLZ
38 46 35.4 392 1 OR9A_DROME
39 46 35.4 504 1 MATK_NEPAL
40 46 35.4 506 1 MATK_CALVU
41 46 35.4 513 1 MATK_CVRRA
42 46 35.4 567 1 EIL3_ARATH
43 46 35.4 635 1 DAL4_YEAST
44 45.5 35.0 688 1 TALA_POVUC
45 45.5 35.0 860 1 LOXA_LYCES

P03369 human immu
Q821.f7 chlamydom
P40328 saccharomyc
P22100 vibrio para
Q01114 mus musculu
P24851 bovine poly
Q01408 neurospora
Q8p1.w4 xanthomonas
P12502 simian immu
P19505 simian immu
P05897 simian immu
P05896 simian immu
Q9b1.k6 lotus japon
Q35611 synechocyst
O66932 aquifex aeo
P17283 chimpanzee
P11640 maize chlor
P39961 saccharomyc
P15833 human immu
P42544 bacterioph
Q9w2u9 drosophila
Q954t2 nepenthes a
O47143 calluna vul
Q8w1.v4 cyrilla rac
Q23116 arabidopsis
Q04895 saccharomyc
P03072 polyomaviru
P38415 lycopersico

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 37.4528 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-8

Perfect score: 130

Sequence: 1 KETWETWETNSQPKRKV 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL_25:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mrc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1 64.5 49.6 433 15 Q79787 Q79787 human immun
2 63 48.5 793 17 Q8TVU1 Q8TVU1 methanopyru
3 61.5 47.3 212 15 Q9WGU7 Q9WGU7 human immun
4 61.5 47.3 225 15 Q98GV3 Q98GV3 human immun
5 61.5 47.3 236 15 Q9WGX3 Q9WGX3 human immun
6 61.5 47.3 237 15 Q9WGV0 Q9WGV0 human immun
7 61.5 47.3 237 15 Q9WGV3 Q9WGV3 human immun
8 61.5 47.3 237 15 Q9WGV7 Q9WGV7 human immun
9 61.5 47.3 237 15 Q9WGV5 Q9WGV5 human immun
10 61.5 47.3 237 15 Q9WGV0 Q9WGV0 human immun
11 61.5 47.3 237 15 Q9WGV5 Q9WGV5 human immun
12 61.5 47.3 237 15 Q9WGV9 Q9WGV9 human immun
13 61.5 47.3 237 15 Q9WGH5 Q9WGH5 human immun
14 61.5 47.3 237 15 Q9WGU0 Q9WGU0 human immun
15 61.5 47.3 237 15 Q9WGX6 Q9WGX6 human immun
16 61.5 47.3 237 15 Q9WGX2 Q9WGX2 human immun
17 61.5 47.3 237 15 Q9WGX5 Q9WGX5 human immun
18 61.5 47.3 237 15 Q9WGW1 Q9WGW1 human immun
19 61.5 47.3 237 15 Q9WGV2 Q9WGV2 human immun
20 61.5 47.3 237 15 Q9WGU8 Q9WGU8 human immun
21 61.5 47.3 237 15 Q9WGW6 Q9WGW6 human immun
22 61.5 47.3 237 15 Q9WGV6 Q9WGV6 human immun
23 61.5 47.3 237 15 Q9WGV8 Q9WGV8 human immun
24 61.5 47.3 237 15 Q9WGW3 Q9WGW3 human immun
25 61.5 47.3 237 15 Q9WGW4 Q9WGW4 human immun
26 61.5 47.3 237 15 Q9WGV1 Q9WGV1 human immun
27 61.5 47.3 237 15 Q9WGV4 Q9WGV4 human immun
28 61.5 47.3 514 15 Q9DLJ8 Q9DLJ8 human immun
29 61.5 47.3 519 15 Q9IDI3 Q9IDI3 human immun
30 61.5 47.3 523 15 Q9IDI9 Q9IDI9 human immun
31 61.5 47.3 523 15 Q9IDC7 Q9IDC7 human immun
32 61.5 47.3 523 15 Q9IDB6 Q9IDB6 human immun
33 61.5 47.3 523 15 Q9IDB2 Q9IDB2 human immun
34 61.5 47.3 523 15 Q9IDF2 Q9IDF2 human immun
35 61.5 47.3 523 15 Q9IDB0 Q9IDB0 human immun
36 61.5 47.3 524 15 Q9IDJ7 Q9IDJ7 human immun
37 61.5 47.3 524 15 Q9IDI8 Q9IDI8 human immun
38 61.5 47.3 524 15 Q9IDI7 Q9IDI7 human immun
39 61.5 47.3 524 15 Q9IDD1 Q9IDD1 human immun
40 61.5 47.3 524 15 Q9IDI6 Q9IDI6 human immun
41 61.5 47.3 524 15 Q9IDB8 Q9IDB8 human immun
42 61.5 47.3 524 15 Q9IDI2 Q9IDI2 human immun
43 61.5 47.3 524 15 Q9IDI4 Q9IDI4 human immun
44 61.5 47.3 524 15 Q9IDI5 Q9IDI5 human immun
45 61.5 47.3 524 15 Q9IDD2 Q9IDD2 human immun

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 13:31:13 ; Search time 53.0189 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRKV 20
Scoring table: BLOSUM62
Gapcp 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	20	5	ABB77673
2	116	94.3	20	5	ABB77672
3	106	86.2	21	5	ABG78995
4	106	86.2	21	5	ABB77693
5	106	86.2	21	5	ABB77671
6	106	86.2	21	7	ADB68484
7	106	86.2	21	7	ADC22460
8	102	82.9	19	5	ABB77699
	96	78.0	20	5	ABB77694

10 95 77.2 19 5 ABB10106 Peptide t
11 94 76.4 21 5 ABB77674 Peptide t
12 84 68.3 21 5 ABB77678 Generic p
13 79 64.2 11 5 ABB77695 Peptide t
14 79 64.2 12 5 ABB77689 Hydrophob
15 79 64.2 12 5 ABB77676 Cell-targ
16 79 64.2 19 5 ABB77676 Peptide t
17 79 64.2 26 5 ABB77676 Peptide t
18 77 62.6 19 5 ABB77675 Chimeric
19 73 59.3 17 5 ABB77667 Peptide t
20 69 56.1 17 5 ABB77692 Peptide t
21 69 56.1 18 5 ABB77666 Peptide t
22 69 56.1 19 5 ABB77668 Peptide t
23 69 56.1 19 5 ABB77698 Peptide t
24 69 56.1 19 5 ABB77669 Peptide t
25 69 56.1 20 5 ABB77679 Generic p
26 64 52.0 19 5 ABB77670 Peptide t
27 57.5 46.7 10 5 ABB77671 HIV-1 BHL
28 57.5 46.7 21 5 ABB77676 Peptide p
29 57.5 46.7 21 5 ABB77665 Peptide t
30 57.5 46.7 25 5 ABB77674 Retroinhi
31 57.5 46.7 430 5 ABB77655 Protein #
32 57.5 46.7 560 4 ABB84201 Amino aci
33 57.5 46.7 560 6 AAG79973 P2C/C38S/
34 57.5 46.7 560 7 ADE28023 HIV-1 RT
35 57.5 46.7 562 6 ABR44741 Plasmid p
36 57.5 46.7 562 6 ABR44740 Plasmid p
37 57.5 46.7 565 6 ABR44743 Plasmid 7
38 57.5 46.7 724 5 AAU1869 HIV pol p
39 57.5 46.7 739 5 AAU1874 HIV pol p
40 57.5 46.7 760 1 AAP94510 Sequence
41 57.5 46.7 850 4 AAEO4792 Human imm
42 57.5 46.7 850 4 AAEO4791 Human imm
43 57.5 46.7 850 5 ADE71141 Codon opt
44 57.5 46.7 850 5 ADE71143 Inactivat
45 57.5 46.7 850 6 ABU63365 HIV-1 wil

ALIGNMENTS

RESULT 1
ID ABE77673 standard; peptide; 20 AA.
XX ABE77673;
AC ABE77673;
XX
DE 01-JUL-2002 (first entry)
XX
DT Peptide transfection agent Pep-2.2.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.

XX 07-FEB-2002.
PD
XX
XX 26-JUL-2001; 2001WO-US023406.
PF
XX
XX 31-JUL-2000; 2000US-0221932P.
PR
XX
XX (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
XX Divida G, Morris M, Mary J, Heitz F, Fernandez J, Archdeacon J;
PI Horroorp K;
FI
XX
XX WPI; 2002-329441/36.
DR
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
PT
XX Claim 12; Page 17; 156pp; English.
PS
XX The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they have particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.2
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 123; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETWETWMTASQPKRKV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KETWETWMTASQPKRKV 20

Search completed: March 1, 2004, 16:55:55
Job time : 33.0189 secs

hypothetical prote
hypothetical prote
probable transcrip
hypothetical prote
spindolin-related
ethylene-insensiti
reverse transcript
hypothetical prote
hypothetical prote
pol polyprotein -
HIV-1 retropepsin
hypothetical prote
probable membrane
probable hydrolase
hypothetical prote
hypothetical prote
plus fringe glycop
homeotic protein C
homeotic protein C
conserved hypotet
hypothetical prote
conserved hypotet
chloride peroxidas
hypothetical prote
MFS permease (limpo
acetolactate synth
probable transport
large f antigen -
poly-beta-hydroxyb
hypothetical prote
callose synthase c
hypothetical prote

14 49 39.8 463 2 T48116
15 48 39.0 1143 2 T22952
16 47 38.2 197 2 F70622
17 47 38.2 305 2 A83340
18 47 38.2 402 2 F82495
19 47 38.2 567 2 F96764
20 46.5 37.8 111 2 A82530
21 46.5 37.8 559 2 A47175
22 46.5 37.8 894 2 T27007
23 46.5 37.8 912 2 S33980
24 46.5 37.8 1003 1 GNMW42
25 46 37.4 289 2 F83405
26 46 37.4 451 2 T37833
27 46 37.4 507 2 T35677
28 46 37.4 563 2 B70918
29 46 37.4 710 2 T25734
30 46 37.4 823 2 T08092
31 45.5 37.0 862 2 B53689
32 45.5 37.0 1332 1 T48314
33 45 36.6 130 2 A82599
34 45 36.6 178 2 H83349
35 45 36.6 211 2 D69529
36 45 36.6 321 1 A28557
37 45 36.6 334 2 T49195
38 45 36.6 535 2 A2710
39 45 36.6 573 1 C64131
40 45 36.6 583 2 F97492
41 45 36.6 586 1 TVRFBP
42 45 36.6 619 2 AH2773
43 45 36.6 637 2 F97553
44 45 36.6 1963 2 T49914
45 44.5 36.2 226 2 T20645

Search completed: March 1, 2004, 19:34:33
Job time : 15:2041 secs

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OM protein - protein search, using sw model
Run on: March 1, 2004, 16:46:26 ; Search time 13.1132 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-9148-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKKRV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues 283366

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57.5	46.7	559	2 B47175	reverse transcript
2	57.5	46.7	1003	1 GNMWLV	HIV-1 retropepsin
3	57.5	46.7	1003	1 B44001	HIV-1 retropepsin
4	57.5	46.7	1003	2 T09440	pol polyprotein -
5	57.5	46.7	1012	1 GNMWVL	HIV-1 retropepsin
6	57.5	46.7	1015	1 GNMWH3	HIV-1 retropepsin
7	52.5	42.7	902	2 T01668	pol polyprotein -
8	52.5	42.7	1002	2 S54378	pol polyprotein -
9	52	42.3	413	2 C91229	hypothetical prote
10	52	42.3	413	2 B86076	hypothetical prote
11	52	42.3	418	2 S40824	hypothetical 48k p
12	51.5	41.9	1002	1 GNLJND	HIV-1 retropepsin
13	51	41.5	849	2 D82510	chitinase VCA0027

OK protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 8.11321 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRKV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57.5	46.7	1003	POL_HV1H2	P04585 human immun
2	57.5	46.7	1003	POL_HV1Y2	P35963 human immun
3	57.5	46.7	1006	POL_HV1YN	P05961 human immun
4	57.5	46.7	1007	POL_HV1UR	P20875 human immun
5	57.5	46.7	1015	POL_HV1B1	P03366 human immun
6	57.5	46.7	1015	POL_HV1B5	P04587 human immun
7	57.5	46.7	1015	POL_HV1BR	P03367 human immun
8	57.5	46.7	1015	POL_HV1PV	P03368 human immun
9	52.5	42.7	1002	POL_HV1EL	P04589 human immun
10	52.5	42.7	1002	POL_HV1VA	P04588 human immun
11	52.5	42.7	1002	POL_HV1RH	P05959 human immun
12	52.5	42.7	1002	POL_HV1Z2	P12499 human immun
13	52.5	42.7	1003	POL_HV1NS	P12497 human immun
14	52.5	42.7	1003	POL_HV1OY	P20892 human immun
15	52	42.3	413	YIHS_ECOLI	P32140 escherictia
16	51.5	41.9	1002	POL_HV1ND	P18802 human immun
17	47	38.2	567	EIL3_ARATH	O23116 arabidopsis

18	46.5	37.8	1002	POL_HV1U4	P24740 human immun
19	46.5	37.8	1003	POL_HV1A2	P03369 human immun
20	46	37.4	78	Y009_BFL2	P42344 bacterioph
21	46	37.4	628	EING_ARATH	O24606 arabidopsi
22	45.5	37.0	860	LOXA_LYCES	P38415 lycopersico
23	45.5	37.0	862	CUTI_RAT	P53565 rattus norv
24	45.5	37.0	1395	CUTI_MOUSE	P53564 mus musculu
25	45	36.6	176	CYTI_STOHE	P81662 stochactis
26	45	36.6	211	YMG6_ARCFU	O28047 archaeglob
27	45	36.6	373	PRXC_GALFU	P04963 caldionmyc
28	45	36.6	518	EIL2_ARATH	O23115 arabidopsi
29	45	36.6	573	ILVI_HAEIN	P43261 haemophilus
30	45	36.6	586	TALA_POVBO	P24851 bovine poly
31	45	36.6	1136	NOS2_CHICK	Q90703 gallus gall
32	45	36.6	1559	STCJ_EMENI	Q00681 emericeila
33	44.5	36.2	861	LOX1_SOLTU	P37831 solanum tub
34	44	35.8	400	GUN5_BACAG	O85465 bacillus ag
35	44	35.8	409	GUN2_BACS4	P06565 bacillus sp
36	44	35.8	495	RT16_MYXXA	P23072 myxococcus
37	44	35.8	488	GUNI_BACS4	P06566 bacillus sp
38	44	35.8	565	MOBA_BIFLO	Q8gn32 bifidobacte
39	44	35.8	964	RRPO_MQAV	P11640 maize chlor
40	44	35.8	1019	POL_SIVS4	P12502 simian immu
41	44	35.8	1022	POL_SIVSP	P18505 simian immu
42	44	35.8	1054	POL_SIVMK	P05897 simian immu
43	44	35.8	1056	POL_SIVM1	P05896 simian immu
44	44	35.8	1171	ZBE4_HUMAN	O75132 homo sapien
45	44	35.8	1196	XPG_XENLA	P14629 xenopus lae

Search completed: March 1, 2004, 19:25:05
Job time : 9.11321 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 37.4528 Seconds
(without alignments)
169.486 Million cell updates/sec

Title: US-09-915-914B-9
Perfect score: 123
Sequence: 1 KETWETWTEASQPKRRKY 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protein:*
- 12: sp_virus:*
- 13: sp_vertibrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description
--------	-------	-----	-------	-------	--------	----	----	-------------

1	64	52.0	793	17	Q8TVU1	Q8TVU1	methanopyru
2	60.5	49.2	433	15	Q79787	Q79787	human immu
3	60.5	49.2	1433	15	Q8AE56	Q8AE56	human immu
4	60	48.8	281	16	Q7U8T9	Q7U8T9	synthetococ
5	59	48.0	66	5	Q9BFC0	Q9BFC0	corus tessu
6	57.5	46.7	212	15	Q9WGU7	Q9WGU7	human immu
7	57.5	46.7	225	15	Q998V3	Q998V3	human immu
8	57.5	46.7	236	15	Q9WGX3	Q9WGX3	human immu
9	57.5	46.7	237	15	Q9WGU0	Q9WGU0	human immu
10	57.5	46.7	237	15	Q9WGV3	Q9WGV3	human immu
11	57.5	46.7	237	15	Q9WGV7	Q9WGV7	human immu
12	57.5	46.7	237	15	Q9WGW5	Q9WGW5	human immu
13	57.5	46.7	237	15	Q9WGW0	Q9WGW0	human immu
14	57.5	46.7	237	15	Q9WGV5	Q9WGV5	human immu
15	57.5	46.7	237	15	Q9WGV9	Q9WGV9	human immu
16	57.5	46.7	237	15	Q9W8H5	Q9W8H5	human immu
17	57.5	46.7	237	15	Q9W9U0	Q9W9U0	human immu
18	57.5	46.7	237	15	Q9WGX6	Q9WGX6	human immu
19	57.5	46.7	237	15	Q9WGW2	Q9WGW2	human immu
20	57.5	46.7	237	15	Q9WGX5	Q9WGX5	human immu
21	57.5	46.7	237	15	Q9WGW1	Q9WGW1	human immu
22	57.5	46.7	237	15	Q9WGV2	Q9WGV2	human immu
23	57.5	46.7	237	15	Q9WGV8	Q9WGV8	human immu
24	57.5	46.7	237	15	Q9WGV6	Q9WGV6	human immu
25	57.5	46.7	237	15	Q9WGV6	Q9WGV6	human immu
26	57.5	46.7	237	15	Q9WGV8	Q9WGV8	human immu
27	57.5	46.7	237	15	Q9WGW3	Q9WGW3	human immu
28	57.5	46.7	237	15	Q9WGW4	Q9WGW4	human immu
29	57.5	46.7	237	15	Q9WGV1	Q9WGV1	human immu
30	57.5	46.7	237	15	Q9WGV4	Q9WGV4	human immu
31	57.5	46.7	514	15	Q9DLJ8	Q9DLJ8	human immu
32	57.5	46.7	519	15	Q9ID13	Q9ID13	human immu
33	57.5	46.7	523	15	Q9ID19	Q9ID19	human immu
34	57.5	46.7	523	15	Q9IDC7	Q9IDC7	human immu
35	57.5	46.7	523	15	Q9IDB6	Q9IDB6	human immu
36	57.5	46.7	523	15	Q9IDB2	Q9IDB2	human immu
37	57.5	46.7	523	15	Q9IDF2	Q9IDF2	human immu
38	57.5	46.7	523	15	Q9IDB0	Q9IDB0	human immu
39	57.5	46.7	524	15	Q9IDJ7	Q9IDJ7	human immu
40	57.5	46.7	524	15	Q9ID18	Q9ID18	human immu
41	57.5	46.7	524	15	Q9ID17	Q9ID17	human immu
42	57.5	46.7	524	15	Q9IDD1	Q9IDD1	human immu
43	57.5	46.7	524	15	Q9ID16	Q9ID16	human immu
44	57.5	46.7	524	15	Q9IDB8	Q9IDB8	human immu
45	57.5	46.7	524	15	Q9ID12	Q9ID12	human immu

Search completed: March 1, 2004, 19:31:58

Job time : 37.4528 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 13:31:13 ; Search time 55.6698 seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-10
Perfect score: 135
Sequence: 1 KETWEIWEIWSQPKKRV 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	21	5 ABB77674	Abb77674 Peptide t
2	123	91.1	21	5 ABG78995	Abg78995 Cell pene
3	123	91.1	21	5 ABB77693	Abb77693 Peptide t
4	123	91.1	21	5 ABB77671	Abb77671 Peptide t
5	123	91.1	21	7 ABB68484	Abb68484 Peptide s
6	123	91.1	21	7 ADC22460	ADC22460 Protein-d
7	120	88.9	19	5 ABB77676	Abb77676 Peptide t
8	117.5	87.0	20	5 ABB77694	Abb77694 Peptide t
9	111	82.2	19	5 ABB10106	Abb10106 Peptide t

10	108	80.0	19	5 ABB77675	Abb77675 Peptide t
11	108	80.0	20	5 ABB77672	Abb77672 Peptide t
12	97	71.9	19	5 ABB77699	Abb77699 Peptide t
13	94	69.6	20	5 ABB77673	Abb77673 Peptide t
14	90	66.7	21	5 ABB77678	Abb77678 Generic p
15	78	57.8	12	5 ABB77689	Abb77689 Hydrophob
16	78	57.8	12	5 ABP56174	ABP56174 Cell-targ
17	78	57.8	26	5 ABP56200	ABP56200 Chimeric
18	74	54.8	19	5 ABB77670	Abb77670 Peptide t
19	69	51.1	11	5 ABB77695	Abb77695 Peptide t
20	63	46.7	17	5 ABB77667	Abb77667 Peptide t
21	62	45.9	286	3 AAG54774	Aag54774 Arabidops
22	62	45.9	383	3 AAG42073	Aag42073 Arabidops
23	62	45.9	432	3 AAG42072	Aag42072 Arabidops
24	62	45.9	435	3 AAG42071	Aag42071 Arabidops
25	59	43.7	9	5 ABB77692	Abb77692 Peptide t
26	59	43.7	18	5 ABB77666	Abb77666 Peptide t
27	59	43.7	19	5 ABB77668	Abb77668 Peptide t
28	59	43.7	19	5 ABB77698	Abb77698 Peptide t
29	59	43.7	19	5 ABB77669	Abb77669 Peptide t
30	59	43.7	20	5 ABB77679	Abb77679 Generic p
31	57.5	42.6	20	2 AAR57412	Aar57412 Peptide f
32	57.5	42.6	89	5 ABR40497	AbR40497 Human sec
33	57.5	42.6	89	5 ABR40420	AbR40420 Human sec
34	57	42.2	418	3 AAB35809	Aab35809 Mannose i
35	57	42.2	496	4 ABG25893	Abg25893 Novel hum
36	57	42.2	928	4 ABG30068	Abg30068 Novel hum
37	57	42.2	928	4 ABG29926	Abg29926 Novel hum
38	56	41.5	10	5 ABB77696	Abb77696 Peptide t
39	56	41.5	16	2 AAW91048	Aaw91048 Internali
40	56	41.5	16	3 AAB27062	Aab27062 Beta-Cate
41	56	41.5	16	3 AAB35696	Aab35696 Peptide a
42	56	41.5	16	3 AAB03929	Aab03929 Internali
43	56	41.5	27	5 ABG78990	Abg78990 Cell pene
44	56	41.5	27	5 AAU78348	Aau78348 Signal se
45	56	41.5	27	5 ABG75506	Abg75506 Signal-se

ALIGNMENTS

RESULT 1
ABB77674
ID ABB77674 standard; peptide; 21 AA.

XX	AC	ABB77674;
XX	DT	01-JUL-2002 (first entry)
XX	DE	Peptide transfection agent Pep-2.3.
XX	KW	Intracellular delivery; transfection agent; cancer; infectious disease;
XX	XX	peptide vector.
XX	OS	Synthetic.
XX	PN	W0200210201-A2.

XX 07-FEB-2002.
XX
XX 26-JUL-2001; 2001WO-US023406.
XX
XX 31-JUL-2000; 2000US-0221932P.
XX
XX (ACTI-) ACTIVE MOTIF.
XX (CNRS) CENT NAT RECH SCI.
XX
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
XX WPI; 2002-329441/36.
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
XX Claim 12; Page 17; 156pp; English.
XX

CC The invention relates to a transfection agent comprising a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.3

XX SQ Sequence 21 AA;
Query Match 100.0%; Score 135; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETWETWETWSQPKKKRV 21
|||||

Db 1 KETWETWETWSQPKKKRV 21
|||||

Search completed: March 1, 2004, 16:55:57
Job time : 57.6698 secs

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OK protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 13.7689 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-10
Perfect score: 135
Sequence: 1 KETWETWETWSQPKKKRV 21

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	58.5	43.3	688	1	TVVPTJ	large T antigen -
2	58	43.0	691	1	TVVPTA	large T antigen -
3	58	43.0	695	1	TVVPTB	large T antigen -
4	57	42.2	418	2	S40824	hypothetical 48K p
5	56.5	41.9	894	2	T27007	hypothetical prote
6	54.5	40.4	708	1	TVVPT4	large T antigen -
7	54	40.0	374	2	AG0937	hypothetical prote
8	54	40.0	413	2	C91229	hypothetical prote
9	54	40.0	413	2	B86076	hypothetical prote
10	51	37.8	435	2	D71857	hypothetical prote
11	51	37.8	435	2	B64658	hypothetical prote
12	51	37.8	519	2	E82932	spermidine/putresc
13	51	37.8	559	2	B47175	reverse transcript

14 51 37.8 965 2 JQ0058
15 51 37.8 1002 1 GNLJND
16 51 37.8 1002 2 S53378
17 51 37.8 1003 1 GNLWLV
18 51 37.8 1003 1 B4001
19 51 37.8 1003 2 T09440
20 51 37.8 1012 1 GNLWVL
21 51 37.8 1015 1 GNLWH3
22 50.5 37.8 1431 2 B8286
23 50.5 37.4 1469 2 H96622
24 50 37.0 455 2 T48973
25 49 36.3 200 2 T42547
26 49 36.3 264 2 F71466
27 49 36.3 629 2 T05099
28 48.5 35.9 188 2 A75382
29 48.5 35.9 239 2 C84505
30 48.5 35.9 331 2 A61046
31 48.5 35.9 472 2 T41694
32 48.5 35.9 692 2 H70362
33 48.5 35.9 770 2 S75042
34 48.5 35.9 794 2 S0687
35 48.5 35.9 1032 2 S12153
36 48.5 35.9 1034 1 GNLJCA
37 48.5 35.9 1035 1 GNLJGG
38 48.5 35.9 1036 1 GNLJG2
39 48.5 35.9 1055 1 GNLJST
40 48 35.6 45 2 C82233
41 48 35.6 338 2 A82890
42 48 35.6 486 2 F64204
43 48 35.6 586 1 TVVPP
44 48 35.6 652 2 T34497
45 48 35.6 935 2 T45778

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 8.51887 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-10
Perfect score: 135
Sequence: 1 KETWEIWTWTSQPKKRYK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: March 1, 2004, 19:34:34

Job time : 14.8598 secs

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.5	43.3	688	1	TALA_POVUC
2	58	43.0	691	1	TALA_POVBA
3	58	43.0	695	1	TALA_POVBK
4	57	42.2	413	1	YIHS_ECOLI
5	54.5	40.4	708	1	TALA_SV40
6	51	37.8	964	1	RRPO_MCMV
7	51	37.8	1002	1	POL_HVIEL
8	51	37.8	1002	1	POL_HVIND
9	51	37.8	1002	1	POL_HVIZ2
10	51	37.8	1003	1	POL_HVIH2
11	51	37.8	1003	1	POL_HVIY2
12	51	37.8	1007	1	POL_HVIJR
13	51	37.8	1015	1	POL_HVIB1
14	51	37.8	1015	1	POL_HVIB5
15	51	37.8	1015	1	POL_HVIBR
16	51	37.8	1015	1	POL_HVIPV
17	50	37.0	1006	1	POL_HVIMN
					P03072 polyomaviru
					P14999 polyomaviru
					P03071 polyomaviru
					P32140 escherichia
					P03070 simian viru
					P11640 maize chlor
					P04589 human immun
					P18502 human immun
					P12499 human immun
					P04585 human immun
					P35963 human immun
					P20875 human immun
					P03566 human immun
					P04587 human immun
					P03367 human immun
					P03368 human immun
					P05961 human immun

18 48.5 35.9 692 1 PHSG_AQUAE
19 48.5 35.9 794 1 YE14_YEAST
20 48.5 35.9 1034 1 POL_HV2CA
21 48.5 35.9 1035 1 POL_HV2KR
22 48.5 35.9 1035 1 POL_HV2NZ
23 48.5 35.9 1033 1 POL_HV2SB
24 48.5 35.9 1036 1 POL_HV2RO
25 48.5 35.9 1049 1 POL_HV2G1
26 48.5 35.9 1055 1 POL_HV2ST
27 48.5 35.9 1073 1 POL_HV2D1
28 48.5 35.9 1142 1 POL_HV2BE
29 48 35.6 41 1 LPW_VIBPA
30 48 35.6 176 1 CYT1_STOHE
31 48 35.6 559 1 POTA_MYGE
32 48 35.6 586 1 TALA_POVBO
33 47.5 35.2 355 1 HKM1_LYCES
34 47.5 35.2 398 1 HKM1_ARATH
35 47.5 35.2 1585 1 YQBO_BACSU
36 47 34.8 336 1 SIFA_SALTY
37 47 34.8 504 1 MATK_NEPAL
38 47 34.8 506 1 MATK_CALVU
39 47 34.8 508 1 MATK_LOTJA
40 47 34.8 560 1 POTA_MYCPN
41 46.5 34.4 315 1 SECF_SYNY3
42 46.5 34.4 568 1 PHAC_CHRVO
43 46 34.1 200 1 UL55_HSVEB
44 46 34.1 502 1 MATK_VACVI
45 46 34.1 508 1 MATK_LOTPU

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMEL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	63	46.7	793	17	Q8TVU1	Q8TVU1 methanopyru
2	61	45.2	431	10	Q8HSC6	Q8HSC6 cryza sativ
3	58.5	43.3	688	12	Q91DF4	Q91DF4 polyomaviru
4	58.5	43.3	688	12	Q8JUC5	Q8JUC5 polyomaviru
5	58.5	43.3	688	12	Q8JUD5	Q8JUD5 polyomaviru
6	58.5	43.3	688	12	Q9WM07	Q9WM07 polyomaviru
7	58.5	43.3	688	12	Q8V6G6	Q8V6G6 polyomaviru
8	58.5	43.3	688	12	Q8JWJ4	Q8JWJ4 polyomaviru
9	58.5	43.3	688	12	Q9WM08	Q9WM08 polyomaviru
10	58.5	43.3	688	12	Q91DF8	Q91DF8 polyomaviru
11	58.5	43.3	688	12	Q8JUD8	Q8JUD8 polyomaviru
12	58.5	43.3	688	12	P88898	P88898 polyomaviru
13	58.5	43.3	688	12	Q8JUE2	Q8JUE2 polyomaviru
14	58.5	43.3	688	12	Q91NL8	Q91NL8 polyomaviru
15	58.5	43.3	688	12	Q91DF5	Q91DF5 polyomaviru
16	58.5	43.3	688	12	Q9W8D4	Q9W8D4 polyomaviru
17	58.5	43.3	688	12	Q91NM2	Q91NM2 polyomaviru
18	58.5	43.3	688	12	Q91NL2	Q91NL2 polyomaviru
19	58.5	43.3	688	12	Q8JZK0	Q8JZK0 polyomaviru
20	58.5	43.3	688	12	Q993Y4	Q993Y4 polyomaviru
21	58.5	43.3	688	12	Q8V6G3	Q8V6G3 polyomaviru
22	58.5	43.3	688	12	Q9WM10	Q9WM10 polyomaviru

Search completed: March 1, 2004, 19:25:06
Job time : 9.51887 secs

23 58.5 43.3 688 12 Q8JUC9
24 58.5 43.3 688 12 Q91D57
25 58.5 43.3 688 12 Q91D52
26 58.5 43.3 688 12 Q8JUC2
27 58.5 43.3 688 12 Q8V6F7
28 58.5 43.3 688 12 Q8JUB9
29 58.5 43.3 688 12 Q8JJK3
30 58.5 43.3 688 12 Q8JPC9
31 58.5 43.3 688 12 Q8JUG1
32 58.5 43.3 688 12 Q91DE6
33 58.5 43.3 688 12 Q8JUB1
34 58.5 43.3 688 12 Q82950
35 58.5 43.3 688 12 Q8JUB6
36 58.5 43.3 688 12 Q8V6H1
37 58.5 43.3 688 12 Q91NL5
38 58.5 43.3 688 12 Q8V6G7
39 58.5 43.3 688 12 Q8JUG4
40 58.5 43.3 688 12 Q8JWJ3
41 58.5 43.3 688 12 Q91DH4
42 58.5 43.3 688 12 Q8JWI7
43 58.5 43.3 688 12 Q8JUC2
44 58.5 43.3 688 12 Q993Y5
45 58.5 43.3 688 12 Q8JUE1

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-11

Perfect score: 119

Sequence: 1 KETWETWTWSQPKKKRV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB ID	Description
		Match	Length			
1	119	100.0	19	5	ABB77675	Abb77675 Peptide t
2	108	90.8	21	5	ABB77674	Abb77674 Peptide t
3	102	85.7	21	5	ABG78995	ABg78995 Cell pene
4	102	85.7	21	5	ABB77693	Abb77693 Peptide t
5	102	85.7	21	5	ABB77671	Abb77671 Peptide t
6	102	85.7	21	7	ADB68484	Adb68484 Peptide s
7	102	85.7	21	7	ADC22460	Adc22460 Protein-d
8	93	78.2	19	5	ABB77676	Abb77676 Peptide t
9	90.5	76.1	20	5	ABB77694	Abb77694 Peptide t

Search completed: March 1, 2004, 19:32:02
Job time : 43.3255 secs

10 87 73.1 20 5 ABB77672 Abb77672 Peptide t
11 84 70.6 19 5 ABB10106 Abb10106 Peptide t
12 77 64.7 20 5 ABB77673 Abb77673 Peptide t
13 71 59.7 21 5 ABB77678 Abb77678 Generic p
14 70 58.8 19 5 ABB77699 Abb77699 Peptide t
15 61.5 51.7 11 5 ABB77695 Abb77695 Peptide t
16 61.5 51.7 12 5 ABB77689 Abb77689 Hydrophob
17 61.5 51.7 12 5 ABP56174 Abp56174 Cell-targ
18 61.5 51.7 26 5 ABP56200 Abp56200 Chimeric
19 56 47.1 10 5 ABB77696 Abb77696 Peptide t
20 56 47.1 27 5 ABG78990 Abg78990 Cell pene
21 56 47.1 27 5 AU78348 Aau78348 Signal se
22 56 47.1 27 5 ABG75506 Abg75506 Signal-se
23 56 47.1 27 5 ABB77685 Abb77685 New pepti
24 56 47.1 27 5 ABB77687 Abb77687 New pepti
25 56 47.1 27 5 ABB81176 Aab81176 Signal se
26 56 47.1 27 5 AA223685 Aae23685 Fluoresce
27 56 47.1 27 6 ABB82542 Abb82542 Signal se
28 56 47.1 27 6 ABR84443 Abbr84443 Chimeric
29 55.5 46.6 17 5 ABB77667 Abb77667 Peptide t
30 54 45.4 115 3 ABB57013 Aab57013 Human pro
31 53.5 45.0 19 5 ABB77670 Abb77670 Peptide t
32 52 43.7 128 3 AAG24065 Aag24065 Arabidops
33 52 43.7 128 3 AAG35083 Aag35083 Arabidops
34 52 43.7 145 3 AAG54796 Aag54796 Arabidops
35 51.5 43.3 9 5 ABB77692 Abb77692 Peptide t
36 51.5 43.3 18 5 ABB77666 Abb77666 Peptide t
37 51.5 43.3 19 5 ABB77668 Abb77668 Peptide t
38 51.5 43.3 19 5 ABB77698 Abb77698 Peptide t
39 51.5 43.3 19 5 ABB77669 Abb77669 Generic p
40 51.5 43.3 20 5 ABB77679 Aab77679 Generic p
41 51 42.9 20 2 AAR57412 Aar57412 Peptide f
42 51 42.9 27 4 AAB85057 Aab85057 N-termina
43 51 42.9 27 5 ABB78712 Abb78712 Peptide M
44 51 42.9 27 5 ABB77681 Abb77681 Peptide v
45 51 42.9 181 6 ABR41729 Abr41729 Human DT

ALIGNMENTS

RESULT 1
ID ABB77675 standard; peptide; 19 AA.
XX
AC ABB77675;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.4.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
FN WO200210201-A2.

XX 07-FEB-2002.
PD
XX
XX 26-JUL-2001; 2001WO-US023406.
PF
XX
XX 31-JUL-2000; 2000US-0221932P.
PR
XX
XX (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
XX WPI; 2002-329441/36.
DR
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
XX Claim 12; Page 17; 156pp; English.
XX
CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.4
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 119; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETWETWWSQPKKKRV 19
| | | | | | | | | | | | | | | | | | | | |
DB 1 KETWETWWSQPKKKRV 19

Search completed: March 1, 2004, 16:55:58
Job time : 51.3679 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-11

Perfect score: 119
Sequence: 1 KETWETWTSQPKKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 9619326 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR78: +
1: pir1: +
2: pir2: +
3: pir3: +
4: pir4: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	45.4	325	2 JC7560	cellulase (EC 3.2.
2	54	45.4	325	2 G70421	probable endogluc
3	54	45.4	472	2 T41684	probable sterol o-
4	53	44.5	142	2 S25757	cytochrome-c oxida
5	51	42.9	118	1 W4MLB2	E4 protein - bovin
6	51	42.9	298	2 B71572	hypothetical prote
7	51	42.9	368	2 E97198	probable enzyme wi
8	51	42.9	376	1 C64135	ribonucleoside-dip
9	50	42.0	160	2 C69900	hypothetical prote
10	50	42.0	308	2 S58504	reverse transcript
11	49.5	41.6	562	2 S25725	poly(3-hydroxyalka
12	49	41.2	336	2 A82890	hypothetical prote
13	49	41.2	1086	2 T40354	hypothetical prote

14	48.5	40.8	894	2 T27007	hypothetical prote
15	48	40.3	1411	2 T48529	hypothetical prote
16	47.5	39.9	229	2 S60454	glucose starvation
17	47.5	39.9	355	2 T07776	Kn1 like-homeo box
18	47.5	39.9	358	2 D85080	KNAT1 homeobox-lik
19	47.5	39.9	688	1 TWPTJ	large T antigen -
20	47.5	39.9	692	2 H70362	glycogen phosphory
21	47	39.5	159	2 F83733	hypothetical prote
22	47	39.5	178	2 A69090	conserved hypotnet
23	47	39.5	376	2 AH0148	ribonucleoside-dip
24	47	39.5	376	2 G84950	ribonucleoside-dip
25	47	39.5	377	2 D81841	ribonucleoside-dip
26	47	39.5	384	2 G81100	ribonucleoside-dip
27	47	39.5	389	2 D82223	ribonucleoside-dip
28	46.5	39.1	331	2 E82170	peptide ABC transp
29	46	38.7	122	2 S32630	ribonucleoside-dip
30	46	38.7	306	1 WZULEB	E2 protein - bovin
31	46	38.7	376	1 RDEC2R	ribonucleoside-dip
32	46	38.7	376	2 F91018	ribonucleoside-dip
33	46	38.7	376	2 H85862	ribonucleoside-dip
34	46	38.7	376	2 XD0791	ribonucleoside-dip
35	46	38.7	560	2 T32661	hypothetical prote
36	46	38.7	627	2 A70888	hypothetical prote
37	46	38.7	691	1 TVVPAS	large T antigen -
38	46	38.7	695	1 TVVPTB	large T antigen -
39	46	38.7	1315	2 T05300	hypothetical prote
40	45.5	38.2	354	1 C37842	cytochrome P450 -
41	45.5	38.2	459	2 AG1987	cytochrome P450 [i
42	45.5	38.2	766	2 S37894	hypothetical prote
43	45	37.8	228	2 AE2173	hypothetical prote
44	45	37.8	247	2 T26688	hypothetical prote
45	45	37.8	669	2 T32512	hypothetical prote

Search completed: March 1, 2004, 19:34:35
Job time : 13.5485 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-11

Perfect score: 119

Sequence: 1 KETWETWTWSQPKKRRV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	44.5	42	1 COX1_MYTED	P41774 mytilus edu
2	51	42.9	112	1 VE4_BPV2	P11301 bovine pepi
3	51	42.9	375	1 RIR2_HAEIN	P43755 haemophilus
4	47.5	39.9	355	1 HRN1_LYCES	Q41330 lycopersico
5	47.5	39.9	398	1 HKL1_ARATH	P46639 arabidopsis
6	47.5	39.9	688	1 TALA_POVUC	P03072 polynomaviru
7	47.5	39.9	692	1 PHSG_AQUAE	Q86932 aquifex aeo
8	47	39.5	376	1 RIR2_BUCAI	P57275 buchnera ap
9	47	39.5	376	1 RIR2_BUCAP	Q8K9W4 buchnera ap
10	47	39.5	376	1 RIR2_BUCBP	Q89as5 buchnera ap
11	46	38.7	257	1 HIS6_VIBVU	Q8d8g5 vibrio vuln
12	46	38.7	375	1 RIR2_ECOLI	P00453 escherichia
13	46	38.7	375	1 RIR2_SALTY	P37427 salmonella
14	46	38.7	691	1 TALA_POVBA	P14999 polynomaviru
15	46	38.7	695	1 TALA_POVBK	P03071 polynomaviru
16	45.5	38.2	459	1 CPXN_ANASP	P29960 anabaena ap
17	45.5	38.2	766	1 STB6_YEAST	P36085 saccharomyc

18	45	37.8	257	1 HIS6_VIBPA	Q87qk6 vibrio para
19	45	37.8	838	1 REC2_HUMAN	Q96ac6 homo sapien
20	45	37.8	935	1 SR13_HUMAN	Q9y3m8 homo sapien
21	44.5	37.4	384	1 ANX3_HORVU	Q43484 hordeum vul
22	44.5	37.4	569	1 PHAC_CHRVU	Q9zh12 chromobacte
23	44.5	37.4	642	1 NA95_MOUSE	Q9r017 mus musculu
24	44.5	37.4	646	1 NA95_HUMAN	Q9ulx6 homo sapien
25	44	37.0	41	1 LPW_VIBPA	P22100 vibrio para
26	44	37.0	124	1 YE22_RHIME	Q92qb2 rhizobium m
27	44	37.0	288	1 SODN_BACCR	Q81416 bacillus ce
28	44	37.0	406	1 ARGI_HUMAN	Q9net3 homo sapien
29	44	37.0	611	1 PHBC_RHIME	P50176 r poly-beta
30	44	37.0	621	1 ULPI_YEAST	Q02724 saccharomyc
31	44	37.0	781	1 TL22_CHICK	Q9dgb6 gallus gall
32	44	37.0	793	1 TL21_CHICK	Q9dd78 gallus gall
33	44	37.0	995	1 SR13_MOUSE	Q923q2 mus musculu
34	44	37.0	1171	1 ZBE4_HUMAN	Q75132 homo sapien
35	43.5	36.6	361	1 OSHI_ORISA	P46609 oryza sativ
36	43.5	36.6	397	1 HKL2_MALDO	Q04135 malus domes
37	43.5	36.6	398	1 HKL1_MALDO	Q04134 malus domes
38	43	36.1	158	1 SSRP_BIFLO	Q89540 bifidobacte
39	43	36.1	258	1 HIS6_ECOLI	Q8fg48 escherichia
40	43	36.1	258	1 HIS6_ECOLI	P10373 escherichia
41	43	36.1	258	1 HIS6_KLEOX	P45603 klebsiella
42	43	36.1	311	1 CLN6_HUMAN	Q9nww5 homo sapien
43	43	36.1	406	1 KDC2_HUMAN	Q9y2u9 homo sapien
44	43	36.1	557	1 ACEA_YEAST	P28240 saccharomyc
45	43	36.1	574	1 HEMA_INEMD	P03461 influenza b

Search completed: March 1, 2004, 19:25:08

Job time : 9.70755 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-11
Perfect score: 119
Sequence: 1 KETWETWTSQKKRKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1:	sp.archaea:
2:	sp.bacteria:
3:	sp.fungi:
4:	sp.human:
5:	sp.invertebrate:
6:	sp.mammal:
7:	sp.mhc:
8:	sp.organelle:
9:	sp.phage:
10:	sp.plant:
11:	sp.rodent:
12:	sp.virus:
13:	sp vertebrate:
14:	sp.unclassified:
15:	sp.rvivirus:
16:	sp.bacteriap:
17:	sp.archaeap:

1	54	45.4	325	16	067401
2	54	45.4	472	3	Q9U82
3	53	44.5	49	8	Q9TD66
4	53	44.5	1417	10	Q9RJ09
5	51	42.9	103	12	Q68353
6	51	42.9	238	16	Q92KL2
7	51	42.9	368	16	Q97GE6
8	51	42.9	376	16	Q9CMT9
9	51	42.9	376	16	Q7VKX9
10	50	42.0	98	13	Q8AV23
11	50	42.0	160	16	Q34637
12	50	42.0	431	10	Q8H8C6
13	50	42.0	432	4	Q8H7M8
14	50	42.0	568	8	Q94L24
15	50	42.0	1412	10	Q7X6H6
16	49.5	41.6	562	2	Q33049
17	49	41.2	338	16	Q9PQ39
18	49	41.2	391	16	Q8A7H7
19	49	41.2	1086	3	Q43043
20	48.5	40.8	894	5	Q9U297
21	48	40.3	198	5	Q9VXX2
22	48	40.3	217	10	Q856K8
23	48	40.3	244	11	Q95QF4
24	48	40.3	1408	10	Q9LDE8
25	48	40.3	1411	10	Q9LYG0
26	47.5	39.9	229	10	Q41855
27	47.5	39.9	400	10	Q85319
28	47.5	39.9	400	10	Q853M0
29	47.5	39.9	688	12	Q91DF4
30	47.5	39.9	688	12	Q8JUC5
31	47.5	39.9	688	12	Q8JUD5
32	47.5	39.9	688	12	Q9WM07
33	47.5	39.9	688	12	Q8V6G6
34	47.5	39.9	688	12	Q8JWJ4
35	47.5	39.9	688	12	Q9WM08
36	47.5	39.9	688	12	Q91DF8
37	47.5	39.9	688	12	Q8JUD8
38	47.5	39.9	688	12	P88898
39	47.5	39.9	688	12	Q8JUE2
40	47.5	39.9	688	12	Q91NL8
41	47.5	39.9	688	12	Q91DF5
42	47.5	39.9	688	12	Q968D4
43	47.5	39.9	688	12	Q91NM2
44	47.5	39.9	688	12	Q91NL2
45	47.5	39.9	688	12	Q8JZK0

Search completed: March 1, 2004, 19:32:05
Job time : 38.5802 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description

OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-12

Perfect score: 125

Sequence: 1 KWEETWETWSQPKKKRV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep29Jan04:*

1: genesep1980s:*

2: genesep1950s:*

3: genesep2000s:*

4: genesep2001s:*

5: genesep2002s:*

6: genesep2003as:*

7: genesep2003bs:*

8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	19	5 ABB77676	Abb77676 Peptide t
2	120	96.0	21	5 ABB77674	Abb77674 Peptide t
3	108	86.4	21	5 ABG78995	Abg78995 Cell pene
4	108	86.4	21	5 ABB77693	Abb77693 Peptide t
5	108	86.4	21	5 ABB77671	Abb77671 Peptide t
6	108	86.4	21	7 ADB68484	Adb68484 Peptide s
7	108	86.4	21	7 ADC22460	Adc22460 Protein-d
8	105	84.0	19	5 ABB10106	Abb10106 Peptide t
9	102.5	82.0	20	5 ABB77694	Abb77694 Peptide t

10	93	74.4	19	5 ABB77675	Abb77675 Peptide t
11	93	74.4	20	5 ABB77672	Abb77672 Peptide t
12	91	72.8	19	5 ABB77699	Abb77699 Peptide t
13	86	68.8	21	5 ABB77678	Abb77678 Generic p
14	79	63.2	20	5 ABB77673	Abb77673 Peptide t
15	64	51.2	19	5 ABB77670	Abb77670 Peptide t
16	63	50.4	12	5 ABB77699	Abb77699 Hydrophob
17	63	50.4	12	5 ABB77699	Abb77699 Cell-targ
18	63	50.4	26	5 ABB77699	Abb77699 Chimeric
19	61	48.8	16	2 AAW91048	Aaw91048 Internali
20	61	48.8	16	2 AAB27062	Aab27062 Beta-cate
21	61	48.8	16	3 AAB35696	Aab35696 Peptide a
22	61	48.8	16	3 AAB35696	Aab35696 Peptide a
23	57.5	46.0	11	2 AAB35696	Aab35696 Peptide f
24	57	45.6	18	1 AAB35696	Aab35696 Peptide f
25	57	45.6	398	4 AAB35696	Aab35696 Peptide f
26	56	44.8	10	5 ABB77696	Abb77696 Peptide t
27	56	44.8	27	5 ABB77696	Abb77696 Peptide t
28	56	44.8	27	5 ABB77696	Abb77696 Peptide t
29	56	44.8	27	5 ABB77696	Abb77696 Peptide t
30	56	44.8	27	5 ABB77696	Abb77696 Peptide t
31	56	44.8	27	5 ABB77696	Abb77696 Peptide t
32	56	44.8	27	5 ABB77696	Abb77696 Peptide t
33	56	44.8	27	5 ABB77696	Abb77696 Peptide t
34	56	44.8	27	6 ABB82542	Abb82542 Signal se
35	56	44.8	27	6 ABB82542	Abb82542 Signal se
36	55	44.0	16	2 AAW33415	Aaw33415 Trp,Arg a
37	55	44.0	16	6 AAB33896	Aab33896 Drosophil
38	55	44.0	16	6 AAB33896	Aab33896 Drosophil
39	55	44.0	298	4 ABB33815	Abb33815 Human mus
40	55	44.0	298	4 AAB42405	Aab42405 Human pol
41	55	44.0	298	4 AAB42405	Aab42405 Human pol
42	55	44.0	298	6 ABB7135	Abb7135 Novel cen
43	54.5	43.6	136	4 ABB66213	Abb66213 SV40 T an
44	54.5	43.6	708	2 AAY06547	Aay06547 SV40 larg
45	54.5	43.6	708	6 ABR55311	Abr55311 Amino aci

ALIGNMENTS

RESULT 1	ABB77676	ABB77676 standard; peptide; 19 AA.
ID	ABB77676	standard; peptide; 19 AA.
XX	ABB77676	
AC	ABB77676	
DT	01-JUL-2002	(first entry)
XX	ABB77676	
DE	Peptide transfection agent Pep-2.5.	
XX	ABB77676	
KW	Intracellular delivery; transfection agent; cancer; infectious disease; peptide vector.	
XX	ABB77676	
OS	Synthetic.	
PN	W0200210201-A2.	

XX PD 07-FEB-2002.

XX AC

XX AB77674;

XX DT 01-JUL-2002 (first entry)

XX DE 31-JUL-2000; 2000US-0221932P.

XX PA (ACTI-) ACTIVE MOTIF.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

XX PI Horndorp K;

XX DR WPI; 2002-329441/36.

XX PT Transfection agent that comprises a peptide comprising hydrophobic and

XX PT hydrophilic domain and having amino acid residues of specified length is

XX PT useful for a non-covalent association with and transport of a

XX PT heterologous compound into a cell.

XX PS Claim 12; Page 17; 156pp; English.

XX CC The invention relates to a transfection agent comprises a peptide of

XX CC about 16 - 30 amino acids in length. Peptides of the invention comprise a

XX CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

XX CC between the domains and a functional group conjugated to at least one

XX CC terminal of the peptide. Peptides of the invention are useful for a non-

XX CC covalent association with and transport of a heterologous compound into a

XX CC cell. They are also useful for promoting the cellular internalisation of

XX CC at least one member e.g. peptide, proteins, antibodies, their derivatives

XX CC and/or conjugates. They may form part of a pharmaceutical composition to

XX CC deliver the compound selected from a diagnostic or therapeutic compound,

XX CC to treat at least one condition such as cancer or an infectious disease,

XX CC or which targets a cancerous cell or pathogen-infected cell and to

XX CC deliver a peptide or inhibitor that disrupts the activity of at least 5%

XX CC The agent of the invention has a transfection efficiency of at least 5%

XX CC for at least two of the members of the group of the compounds. The agent

XX CC has a good delivery efficiency for a broad spectrum of compounds and cell

XX CC types, has a low toxicity, are easy to handle and easy to formulate in

XX CC conjunction with the many different compound types that it can deliver.

XX CC The peptides are serum sensitive, thus they code particularly well for

XX CC systemic and/or localised in patients. The current sequence represents

XX CC the peptide transfection agent Pep-2.5

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 125; DB 5; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.4e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMWETWETWSQPKKKRV 19

Db 1 KMWETWETWSQPKKKRV 19

|||||

RESULT 2

AB77674

ABB77674 standard; peptide; 21 AA.

ABB77674;

01-JUL-2002 (first entry)

Peptide transfection agent Pep-2.3.

Intracellular delivery; transfection agent; cancer; infectious disease;

peptide vector.

Synthetic.

WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.

(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and

hydrophilic domain and having amino acid residues of specified length is

useful for a non-covalent association with and transport of a

heterologous compound into a cell.

Claim 12; Page 17; 156pp; English.

The invention relates to a transfection agent comprises a peptide of

about 16 - 30 amino acids in length. Peptides of the invention comprise a

hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

between the domains and a functional group conjugated to at least one

terminal of the peptide. Peptides of the invention are useful for a non-

covalent association with and transport of a heterologous compound into a

cell. They are also useful for promoting the cellular internalisation of

at least one member e.g. peptide, proteins, antibodies, their derivatives

and/or conjugates. They may form part of a pharmaceutical composition to

deliver the compound selected from a diagnostic or therapeutic compound,

to treat at least one condition such as cancer or an infectious disease,

or which targets a cancerous cell or pathogen-infected cell and to

deliver a peptide or inhibitor that disrupts the activity of at least 5%

The agent of the invention has a transfection efficiency of at least 5%

for at least two of the members of the group of the compounds. The agent

has a good delivery efficiency for a broad spectrum of compounds and cell

types, has a low toxicity, are easy to handle and easy to formulate in

conjunction with the many different compound types that it can deliver.

The peptides are serum sensitive, thus they code particularly well for

systemic and/or localised in patients. The current sequence represents

the peptide transfection agent Pep-2.3

XX Sequence 21 AA;
SQ

Query Match 96.0%; Score 120; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WWTWETWWSQPKKKRKV 19
Db 4 WWTWETWWSQPKKKRKV 21

Search completed: March 1, 2004, 16:56:00
Job time : 52.3679 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-12
Perfect score: 125
Sequence: 1 KWTWETWWSQPKKKRKV 19

Scoring table: BLASUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	46.4	691	1	TWPTAS
2	58	46.4	695	1	TWPTB
3	57.5	46.0	688	1	TWPTJ
4	54.5	43.6	708	1	TWPT4
5	54	43.2	374	2	AG0537
6	53	42.4	435	2	D71857
7	53	42.4	435	2	B64658
8	51.5	41.2	894	2	T27007
9	51	40.8	519	2	E82932
10	51	40.8	965	2	J00058
11	50	40.0	455	2	T48973
12	50	40.0	2228	2	T14029
13	49.5	39.6	1595	2	B69948

14 49 39.2 200 2 T42547
15 49 39.2 629 2 T05089
16 48.5 38.8 188 2 A75382
17 48.5 38.8 217 2 S42877
18 48.5 38.8 218 2 J04260
19 48.5 38.8 331 2 A61046
20 48 38.4 45 2 C82233
21 48 38.4 115 2 A11891
22 48 38.4 338 2 A82890
23 48 38.4 586 1 TVVPEP
24 48 38.4 652 2 T34457
25 48 38.4 935 2 T48778
26 47.5 38.0 200 2 A72480
27 47.5 38.0 472 2 T41684
28 47.5 38.0 544 2 B84264
29 47 37.6 121 2 T17708
30 47 37.6 371 2 T30292
31 47 37.6 371 2 A08837
32 47 37.6 418 2 S40824
33 47 37.6 475 2 A12439
34 47 37.6 497 2 T47715
35 47 37.6 710 2 T25734
36 47 37.6 753 2 A86736
37 47 37.6 823 2 T08032
38 47 37.6 1103 2 T42022
39 47 37.6 1451 2 B86286
40 47 37.6 1469 2 H96622
41 47 37.6 1711 2 C71625
42 47 37.6 2182 2 T28634
43 47 37.6 2197 2 B71600
44 46.5 37.2 111 2 A82530
45 46.5 37.2 315 2 F95855

gene 4 protein - e
hypothetical prote
hypothetical prote
ribosomal protein
breast basic conse
ecdysone-induced m
hypothetical prote
hypothetical prote
hypothetical prote
large T antigen -
hypothetical prote
hypothetical prote
hypothetical prote
probable sterol o-
glycine betaine tr
hypothetical prote
glucosyl-transfera
probable glycosylt
hypothetical 48K p
hypothetical prote
hypothetical prote
hypothetical prote
plus fringe glycop
probable chitin sy
F9L1.15 protein -
probable ABC trans
variant-specific s
variant-specific s
variant-specific s
hypothetical prote
probable oligopept

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-12
Perfect score: 125
Sequence: 1 KMWETWETWSQPKKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: March 1, 2004, 19:34:36
Job time : 13.5485 secs

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	46.4	691	1	TALA_POVBA
2	58	46.4	695	1	TALA_POVEX
3	57.5	46.0	688	1	TALA_POVJC
4	54.5	43.6	708	1	TALA_SV40
5	51	40.8	964	1	RRPO_MQW
6	49.5	39.6	508	1	MATK_LOTJA
7	49.5	39.6	1585	1	YOBO_BACSU
8	48.5	38.8	218	1	RL13_DROME
9	48.5	38.8	504	1	MATK_NEPAL
10	48.5	38.8	506	1	MATK_CALVO
11	48.5	38.8	508	1	MATK_LOTPU
12	48	38.4	41	1	LEW_VIBPA
13	48	38.4	176	1	CYT1_STOHE
14	48	38.4	586	1	TALA_POVBO
15	47.5	38.0	502	1	MATK_VACVI
16	47.5	38.0	503	1	MATK_VICSA
17	47.5	38.0	503	1	MATK_VICVI

P14999 polyomaviru
P03071 polyomaviru
P03072 polyomaviru
P03070 simian viru
P11640 maize chlor
Q9bbu2 lotus japon
P45931 bacillus su
P41126 drosophila
Q95gt2 nepenthes a
Q47143 callura vul
Q9tkp8 lotus pursh
P22100 vibrio para
P81662 stoichactis
P24851 bovine poly
Q8wi19 vaccinium v
Q8mcj5 vicia sativ
Q8mcj4 vicia villo

18 47.5 38.0 506 1 MATK_LATSA
19 47.5 38.0 506 1 MATK_TRIRP
20 47.5 38.0 506 1 MATK_TRISU
21 47.5 38.0 507 1 MATK_LENCU
22 47.5 38.0 507 1 MATK_LENER
23 47.5 38.0 513 1 MATK_CYBRA
24 47 37.6 413 1 YHS_ECOLI
25 47 37.6 1103 1 CHS6_USMA
26 46.5 37.2 506 1 MATK_LATAP
27 46.5 37.2 506 1 MATK_LATTI
28 46.5 37.2 506 1 MATK_MELAB
29 46.5 37.2 794 1 YE14_YEAST
30 46.5 37.2 1002 1 POL_HV1EL
31 46.5 37.2 1002 1 POL_HV1ND
32 46.5 37.2 1002 1 POL_HV1Z2
33 46.5 37.2 1003 1 POL_HV1H2
34 46.5 37.2 1003 1 POL_HV1Y2
35 46.5 37.2 1007 1 POL_HV1JR
36 46.5 37.2 1015 1 POL_HV1B1
37 46.5 37.2 1015 1 POL_HV1B5
38 46.5 37.2 1015 1 POL_HV1BR
39 46.5 37.2 1015 1 POL_HV1PV
40 46 36.8 78 1 Y009_BPL2
41 46 36.8 200 1 UL55_HSVEB
42 46 36.8 447 1 GNT1_MOUSE
43 46 36.8 447 1 GNT1_RABIT
44 46 36.8 447 1 GNT1_RAT
45 45.5 36.4 355 1 HKM1_LYCES

Search completed: March 1, 2004, 19:25:08
Job time : 7.70755 secs

Q8mer9 lathyrus sa
Q8mem4 trifolium i
Q8mem0 trifolium s
Q8mer6 lens culina
Q8mer5 lens ervoid
Q8wiv4 cyrilla rac
P32140 escherichia
O13395 ustilago ma
Q8mes1 lathyrus ap
Q8mer8 lathyrus ti
Q8mcp5 melilotus a
P39961 saccharomyc
P04589 human immun
P18902 human immun
P12499 human immun
P04365 human immun
P35963 human immun
P20875 human immun
P03366 human immun
P04587 human immun
P03367 human immun
P03368 human immun
P42544 bacterioph
P28963 equine herp
P27808 mus musculu
P27115 oryctolagus
Q09325 rattus norv
Q41330 lycopersico

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-12
Perfect score: 125
Sequence: 1 KMWETWETWSQPKKRV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_misc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
Description					

1	63	50.4	793	17	Q8TVU1	Q8TVU1 methanopyru
2	57.3	46.0	688	12	Q91DF4	Q91df4 polyomaviru
3	57.5	46.0	688	12	Q8JUC5	Q8juc5 polyomaviru
4	57.5	46.0	688	12	Q8JUD5	Q8jud5 polyomaviru
5	57.5	46.0	688	12	Q9WM07	Q9wm07 polyomaviru
6	57.5	46.0	688	12	Q8V6G6	Q8v6g6 polyomaviru
7	57.5	46.0	688	12	Q8JWJ4	Q8jwj4 polyomaviru
8	57.5	46.0	688	12	Q9WM08	Q9wm08 polyomaviru
9	57.5	46.0	688	12	Q91DF8	Q91df8 polyomaviru
10	57.5	46.0	688	12	Q8JUD8	Q8jud8 polyomaviru
11	57.5	46.0	688	12	P88898	P88898 polyomaviru
12	57.5	46.0	688	12	Q8JUE2	Q8jue2 polyomaviru
13	57.5	46.0	688	12	Q91NL8	Q91nl8 polyomaviru
14	57.5	46.0	688	12	Q91DF5	Q91df5 polyomaviru
15	57.5	46.0	688	12	Q9W8D4	Q9w8d4 polyomaviru
16	57.5	46.0	688	12	Q91NM2	Q91nm2 polyomaviru
17	57.5	46.0	688	12	Q91NL2	Q91nl2 polyomaviru
18	57.5	46.0	688	12	Q8JZK0	Q8jzk0 polyomaviru
19	57.5	46.0	688	12	Q993Y4	Q993y4 polyomaviru
20	57.5	46.0	688	12	Q8V6G3	Q8v6g3 polyomaviru
21	57.5	46.0	688	12	Q9WM10	Q9wm10 polyomaviru
22	57.5	46.0	688	12	Q8JUC9	Q8juc9 polyomaviru
23	57.5	46.0	688	12	Q91DG7	Q91dg7 polyomaviru
24	57.5	46.0	688	12	Q91OD2	Q91od2 polyomaviru
25	57.5	46.0	688	12	Q8JZJ2	Q8jzj2 polyomaviru
26	57.5	46.0	688	12	Q8V6F7	Q8v6f7 polyomaviru
27	57.5	46.0	688	12	Q8JUB9	Q8jub9 polyomaviru
28	57.5	46.0	688	12	Q8JJK3	Q8jjk3 polyomaviru
29	57.5	46.0	688	12	Q9DPC9	Q9dpc9 polyomaviru
30	57.5	46.0	688	12	Q9DUG1	Q9dug1 polyomaviru
31	57.5	46.0	688	12	Q91DE6	Q91de6 polyomaviru
32	57.5	46.0	688	12	Q8JUB1	Q8jub1 polyomaviru
33	57.5	46.0	688	12	Q829S0	Q829s0 polyomaviru
34	57.5	46.0	688	12	Q8JUB6	Q8jub6 polyomaviru
35	57.5	46.0	688	12	Q8V6H1	Q8v6h1 polyomaviru
36	57.5	46.0	688	12	Q91NL5	Q91nl5 polyomaviru
37	57.5	46.0	688	12	Q8V6G7	Q8v6g7 polyomaviru
38	57.5	46.0	688	12	Q8DUG4	Q8dug4 polyomaviru
39	57.5	46.0	688	12	Q8JWJ3	Q8jwj3 polyomaviru
40	57.5	46.0	688	12	Q91DH4	Q91dh4 polyomaviru
41	57.5	46.0	688	12	Q8JWI7	Q8jwi7 polyomaviru
42	57.5	46.0	688	12	Q8JUC2	Q8juc2 polyomaviru
43	57.5	46.0	688	12	Q993Y5	Q993y5 polyomaviru
44	57.5	46.0	688	12	Q8JUE1	Q8jue1 polyomaviru
45	57.5	46.0	688	12	Q91DH0	Q91dh0 polyomaviru

Search completed: March 1, 2004, 19:32:06
Job time : 36.5802 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 55.6698 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-1

Perfect score: 134

Sequence: 1 YGFKRRMSQPKETWTWTE 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep29Jan04:*

1: genesep1980s:*

2: genesep1950s:*

3: genesep2000s:*

4: genesep2001s:*

5: genesep2002s:*

6: genesep2003as:*

7: genesep2003bs:*

8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	21	5 ABB77665	Abb77665 Peptide t
2	79.5	59.3	18	5 ABB77666	Abb77666 Peptide t
3	79	59.0	17	5 ABB77667	Abb77667 Peptide t
4	77.5	57.8	25	5 ABB78714	Abb78714 Retroinhl
5	77	57.5	20	5 ABB77679	Abb77679 Generic p
6	75	56.0	19	5 ABB77668	Abb77668 Peptide t
7	73	56.0	19	5 ABB77698	Abb77698 Peptide t
8	73	56.0	19	5 ABB77669	Abb77669 Peptide t
9	74	55.2	1185	5 AAU80135	AAU80135 Chimeric

10	* 74	55.2	1185	6 AAE33407	Aae33407 Chimeric
11	68	50.7	10	5 ABB78711	Abb78711 HIV-1 BH1
12	68	50.7	21	5 ABB78716	Abb78716 Peptide p
13	68	50.7	430	5 ABP4755	Abp47755 Protein #
14	68	50.7	560	4 AAB84201	Aab84201 Amino aci
15	68	50.7	560	6 AAG79973	Aag79973 P20/C38S/
16	68	50.7	560	7 ADE29023	Ade29023 HIV-1 RT
17	68	50.7	562	6 ABR44741	AbR44741 Plasmid p
18	68	50.7	562	6 ABR44740	AbR44740 Plasmid p
19	68	50.7	565	6 ABR44743	AbR44743 Plasmid 7
20	68	50.7	724	5 AAU11869	Aau11869 HIV pol p
21	68	50.7	739	5 AAU11874	Aau11874 HIV pol p
22	68	50.7	760	1 AAP94510	Aap94510 Sequence
23	68	50.7	850	4 AAE04792	Aae04792 Human imm
24	68	50.7	850	4 AAE04791	Aae04791 Human imm
25	68	50.7	850	5 ADE71141	Ade71141 Codon opt
26	68	50.7	850	5 ADE71143	Ade71143 Inactivat
27	68	50.7	850	6 ABU63365	Abu63365 HIV-1 wil
28	68	50.7	850	6 ABU63366	Abu63366 HIV-1 ina
29	68	50.7	873	4 AAE04794	Aae04794 Human tpa
30	68	50.7	875	4 AAE04793	Aae04793 Human tpa
31	68	50.7	875	5 ADE71145	Ade71145 Codon opt
32	68	50.7	875	5 ADE71147	Ade71147 Inactivat
33	68	50.7	875	6 ABU63368	Abu63368 HIV-1 ina
34	68	50.7	875	6 ABU63367	Abu63367 HIV-1 wil
35	68	50.7	902	3 ABU12995	Abu12995 HIV-1 rev
36	68	50.7	912	2 AAR08053	Aar08053 AcNPV-HIV
37	68	50.7	912	2 AAR08057	Aar08057 HIV-1 pol
38	68	50.7	979	4 AAG80980	Aag80980 HIV prote
39	68	50.7	1002	3 AAB69281	Aab69281 HIV-1 non
40	68	50.7	1003	1 AAP60420	Aap60420 Sequence
41	68	50.7	1003	1 AAP70861	Aap70861 Sequence
42	68	50.7	1003	5 AAQ19387	Aaq19387 Lymphaden
43	68	50.7	1003	6 AAO30963	Aao30963 HIV pol p
44	68	50.7	1010	2 AAR91823	Aar91823 Human imm
45	68	50.7	1012	1 AAP61507	Aap61507 Sequence

ALIGNMENTS

RESULT 1
ABB77665
ID ABB77665 standard; peptide; 21 AA.
XX
AC ABB77665;
XX
XX
DT 01-JUL-2002 (first entry)

XX Peptide transfection agent Pep-1.
XX
XX Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
XX
OS Synthetic.
XX
XX W0200210201-A2.

```

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NM protein - protein search, using sw model

Run on:      March 1, 2004, 16:46:26 ; Search time 13.7689 Seconds
              (without alignments)
              146.709 Million cell updates/sec

Title:       US-09-915-914B-1
Perfect score: 134
Sequence:    1 YGFKRRWSQPKETWETWTE 21

Scoring table:  BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:     283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:  283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :     PIR_78:*
              1: Pirl:*
              2: Pir2:*
              3: Pir3:*
              4: Pir4:*

      pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

SUMMARIES



| Result No. | Score | Match | Length | DB | ID     | Description        |
|------------|-------|-------|--------|----|--------|--------------------|
| 1          | 70    | 52.2  | 559    | 2  | B47175 | reverse transcript |
| 2          | 68    | 50.7  | 1003   | 1  | GNWVLV | HIV-1 retropepsin  |
| 3          | 68    | 50.7  | 1003   | 1  | B44001 | HIV-1 retropepsin  |
| 4          | 68    | 50.7  | 1003   | 2  | T09440 | pol polyprotein -  |
| 5          | 68    | 50.7  | 1012   | 1  | GNWVWL | HIV-1 retropepsin  |
| 6          | 68    | 50.7  | 1015   | 1  | GNWVH3 | HIV-1 retropepsin  |
| 7          | 63    | 47.0  | 902    | 2  | T01668 | pol polyprotein -  |
| 8          | 63    | 47.0  | 1002   | 2  | S54378 | pol polyprotein -  |
| 9          | 62    | 46.3  | 1002   | 1  | GNLJND | HIV-1 retropepsin  |
| 10         | 60    | 44.8  | 487    | 4  | S1886  | hypothetical prote |
| 11         | 60    | 44.8  | 492    | 2  | S1885  | probable membrane  |
| 12         | 60    | 44.8  | 528    | 4  | S1887  | hypothetical prote |


```

reverse transcript
 pol polyprotein -
 HIV-1 retropepsin
 hypothetical 7.6K
 HIV-1 retropepsin
 pol polyprotein -
 HIV-1 retropepsin
 HIV-1 retropepsin
 hypothetical prote
 transposase (clone
 hypothetical prote
 S-locus-specific g
 cytochrome P450 ka
 hypothetical prote
 pol polyprotein -
 A-kinase anchoring
 f9Li.15 protein -
 probable ABC trans
 hypothetical prote
 DNA-binding protei
 probable DNA-bind
 subunit of ABC tra
 conserved hypothet
 early E1B 52K prot
 hypothetical prote
 hypothetical prote
 probable membrane
 probable minor str
 hypothetical prote
 hypothetical prote
 HIV-1 retropepsin
 probable glucan sy
 hypothetical prote
 beta-galactosidase

57 42.5 559 2 A47175
 57 42.5 912 2 S33980
 57 42.5 1003 1 GNWAZ
 55 41.0 69 2 JQ1257
 55 41.0 1027 1 GNLJ51
 53 39.6 1058 2 S08436
 52 38.8 1056 1 GNLJG3
 51 38.1 376 2 H82988
 51 37.7 150 2 S36991
 50 37.3 392 2 T19698
 50 37.3 426 2 T14527
 50 37.3 509 2 T51806
 50 37.3 669 2 T13335
 50 37.3 1019 2 T11560
 49.5 36.9 860 2 JCS986
 49.5 36.9 1451 2 B86286
 49.5 36.9 1469 2 H86622
 49 36.6 201 2 T49792
 49 36.6 214 2 AC2726
 49 36.6 229 2 G97507
 49 36.6 234 2 B88934
 49 36.6 303 2 A23201
 49 36.6 472 1 WNAJ36
 49 36.6 535 2 T41384
 49 36.6 633 2 S60408
 49 36.6 669 2 T13640
 49 36.6 670 2 T09274
 49 36.6 670 2 T09205
 49 36.6 1035 1 GNLJG3
 49 36.6 1510 2 C84727
 49 36.6 1878 2 E86189
 48.5 36.2 727 2 T47341

Search completed: March 1, 2004, 19:34:20
 Job time : 16.8598 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 13.7689 Seconds
 (without alignments)
 146.709 Million cell updates/sec

Title: US-09-915-914B-1
 Perfect score: 134
 Sequence: 1 YGFKRRWSQPKETWETWTE 21

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	52.2	559	2 B47175	reverse transcript
2	68	50.7	1003	1 GNWLV	HIV-1 retropepsin
3	68	50.7	1003	1 B44001	HIV-1 retropepsin
4	68	50.7	1003	2 T09440	pol polyprotein -
5	68	50.7	1012	1 GNWVL	HIV-1 retropepsin
6	68	50.7	1015	1 GNWVH3	HIV-1 retropepsin
7	63	47.0	902	2 T01668	pol polyprotein -
8	63	47.0	1002	2 S54378	pol polyprotein -
9	62	46.3	1002	1 GNLJND	HIV-1 retropepsin
10	60	44.8	487	4 S1886	hypothetical prote
11	60	44.8	492	2 S1885	probable membrane
12	60	44.8	528	4 S1887	hypothetical prote
13	59	44.0	420	2 D69769	cellulose synthase

reverse transcript
pol polyprotein -
HIV-1 retropepsin
hypothetical 7.6K
HIV-1 retropepsin
pol polyprotein -
HIV-1 retropepsin
hypothetical prote
transposase (clone
hypothetical prote
S-locus-specific g
cytochrome P450 Ka
hypothetical prote
pol polyprotein -
A-kinase anchoring
F9L1.15 protein -
probable ABC trans
hypothetical prote
DNA-binding protei
probable DNA-bind
subunit of ABC tra
conserved hypothet
early E1B 52K prot
hypothetical prote
probable membrane
probable minor str
hypothetical prote
hypothetical prote
HIV-1 retropepsin
probable glucan sy
hypothetical prote
beta-galactosidase

14 57 42.5 559 2 A47175
15 57 42.5 912 2 S33980
16 57 42.5 1003 1 GNVW22
17 55 41.0 69 2 JQ1237
18 55 41.0 1027 1 GNLJ51
19 53 39.6 1058 2 S08436
20 52 38.8 1056 1 GNLJG3
21 51 38.1 376 2 H82988
22 50.5 37.7 150 2 S36991
23 50 37.3 392 2 T19698
24 50 37.3 426 2 T14327
25 50 37.3 509 2 T31806
26 50 37.3 669 2 T13335
27 50 37.3 1019 2 T11560
28 49.5 36.9 860 2 JCS986
29 49.5 36.9 1451 2 B86286
30 49.5 36.9 1469 2 H96622
31 49 36.6 201 2 T49732
32 49 36.6 214 2 AC2726
33 49 36.6 229 2 G97507
34 49 36.6 234 2 B89934
35 49 36.6 303 2 AE3201
36 49 36.6 472 1 WNA076
37 49 36.6 535 2 T41384
38 49 36.6 633 2 S60408
39 49 36.6 669 2 T13640
40 49 36.6 670 2 T09274
41 49 36.6 670 2 T09205
42 49 36.6 1035 1 GNLJG3
43 49 36.6 1510 2 C84727
44 49 36.6 1878 2 E86189
45 48.5 36.2 727 2 T47541

Search completed: March 1, 2004, 19:34:20
Job time : 16.8598 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 39.3255 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-1
Perfect score: 134
Sequence: 1 YGFKRWSQPKETWTWTE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
---------------	-------	----------------	--------	----	----	-------------

1	73	54.5	1433	15	G8AE23	G8AE23	human	immu
2	70	52.2	539	15	G9PXX1	G9PXX1	human	immu
3	69	51.5	237	15	G9WGW1	G9WGW1	human	immu
4	69	51.5	562	15	G9AAZ9	G9AAZ9	human	immu
5	69	51.5	591	15	G8Q884	G8Q884	human	immu
6	69	51.5	1003	15	G8AC77	G8AC77	human	immu
7	68	50.7	212	15	G9WGU7	G9WGU7	human	immu
8	68	50.7	225	15	G998V3	G998V3	human	immu
9	68	50.7	237	15	G9WGV0	G9WGV0	human	immu
10	68	50.7	237	15	G9WGV3	G9WGV3	human	immu
11	68	50.7	237	15	G9WGV7	G9WGV7	human	immu
12	68	50.7	237	15	G9WGW5	G9WGW5	human	immu
13	68	50.7	237	15	G9WGW0	G9WGW0	human	immu
14	68	50.7	237	15	G9WGV5	G9WGV5	human	immu
15	68	50.7	237	15	G9WGV9	G9WGV9	human	immu
16	68	50.7	237	15	G9W8H5	G9W8H5	human	immu
17	68	50.7	237	15	G9W9U0	G9W9U0	human	immu
18	68	50.7	237	15	G9WGX6	G9WGX6	human	immu
19	68	50.7	237	15	G9WGW2	G9WGW2	human	immu
20	68	50.7	237	15	G9WGX5	G9WGX5	human	immu
21	68	50.7	237	15	G9WGV2	G9WGV2	human	immu
22	68	50.7	237	15	G9WGU8	G9WGU8	human	immu
23	68	50.7	237	15	G9WGW6	G9WGW6	human	immu
24	68	50.7	237	15	G9WGV8	G9WGV8	human	immu
25	68	50.7	237	15	G9WGVH	G9WGVH	human	immu
26	68	50.7	237	15	G9WGW3	G9WGW3	human	immu
27	68	50.7	237	15	G9WGW4	G9WGW4	human	immu
28	68	50.7	237	15	G9WGV1	G9WGV1	human	immu
29	68	50.7	237	15	G9WGV4	G9WGV4	human	immu
30	68	50.7	433	15	G79787	G79787	human	immu
31	68	50.7	514	15	G9DLJ8	G9DLJ8	human	immu
32	68	50.7	519	15	G91D13	G91D13	human	immu
33	68	50.7	523	15	G91D19	G91D19	human	immu
34	68	50.7	523	15	G91DC7	G91DC7	human	immu
35	68	50.7	523	15	G91DB6	G91DB6	human	immu
36	68	50.7	523	15	G91DB2	G91DB2	human	immu
37	68	50.7	523	15	G91DF2	G91DF2	human	immu
38	68	50.7	523	15	G91DB0	G91DB0	human	immu
39	68	50.7	524	15	G91D17	G91D17	human	immu
40	68	50.7	524	15	G91D18	G91D18	human	immu
41	68	50.7	524	15	G91D17	G91D17	human	immu
42	68	50.7	524	15	G91DD1	G91DD1	human	immu
43	68	50.7	524	15	G91D16	G91D16	human	immu
44	68	50.7	524	15	G91DB8	G91DB8	human	immu
45	68	50.7	524	15	G91D12	G91D12	human	immu

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKRRQPTWETWTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:  1586107
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : A_Geneseq_29Jan04.*
1: geneseq1980s.*
2: geneseq1990s.*
```

3: geneseg2001s: *
4: geneseg2001s: *
5: geneseg2002s: *
6: geneseg2003as: *
7: geneseg2003bs: *
8: geneseg2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	120	100.0	18 5	AB577666	Ab577666 Peptide t
2	102.5	85.4	17 5	AB577667	Ab577667 Peptide t
3	99.5	82.9	20 5	AB577679	Ab577679 Generic p
4	97.5	81.2	19 5	AB577668	Ab577668 Peptide t
5	97.5	81.2	19 5	AB577698	Ab577698 Peptide t
6	97.5	81.2	19 5	AB577669	Ab577669 Peptide t
7	79.5	66.2	21 5	AB577665	Ab577665 Peptide t
8	69	57.5	9 5	AB577692	Ab577692 Peptide t
9	69	57.5	11 5	AB577695	Ab577695 Peptide t

Search completed: March 1, 2004, 19:31:49
Job time : 44.3255 secs

XX 07-FEB-2002.

XX 26-JUL-2001; 2001WO-US023406.

XX 31-JUL-2000; 2000US-0221932P.

XX (ACT1-) ACTIVE MOTIF.

XX (CNRS) CENT NAT RECH SCI.

XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

XX Horndorff K;

XX WPI; 2002-329441/36.

XX Transfection agent that comprises a peptide comprising hydrophobic and

XX hydrophilic domain and having amino acid residues of specified length is

XX useful for a non-covalent association with and transport of a

XX heterologous compound into a cell.

XX Claim 12; Page 16; 156pp; English.

XX The invention relates to a transfection agent comprises a peptide of

XX about 16 - 30 amino acids in length. Peptides of the invention comprise a

XX hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

XX between the domains and a functional group conjugated to at least one

XX terminal of the peptide. Peptides of the invention are useful for a non-

XX covalent association with and transport of a heterologous compound into a

XX cell. They are also useful for promoting the cellular internalisation of a

XX cell at least one member e.g. peptide, proteins, antibodies, their derivatives

XX and/or conjugates. They may form part of a pharmaceutical composition to

XX deliver the compound selected from a diagnostic or therapeutic compound,

XX to treat at least one condition such as cancer or an infectious disease,

XX or which targets a cancerous cell or pathogen-infected cell and to

XX deliver a peptide or inhibitor that disrupts the activity of the enzyme.

XX The agent of the invention has a transfection efficiency of at least 5%

XX for at least two of the members of the group of the compounds. The agent

XX has a good delivery efficiency for a broad spectrum of compounds and cell

XX types, has a low toxicity, are easy to handle and easy to formulate in

XX conjunction with the many different compound types that it can deliver.

XX The peptides are serum sensitive, thus they are particularly well for

XX systemic and/or localised in patients. The current sequence represents

XX the peptide transfection agent Pep-1.1

XX Sequence 18 AA;

XX Query Match 100.0%; Score 120; DB 5; Length 18;

XX Best Local Similarity 100.0%; Pred.No.1e-09;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 YGFKRRQPTWETWTE 18

XX 1 YGFKRRQPTWETWTE 18

XX Search completed: March 1, 2004, 16:55:39

XX Job time : 48.717 secs

XX 01-JUL-2002 (first entry)

XX Peptide transfection agent Pep-1.1.

XX Intracellular delivery; transfection agent; cancer; infectious disease;

XX Peptide vector.

XX Synthetic.

XX W0200210201-A2.

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:46:26 ; Search time 11.8019 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKRRQPTWETWTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues 283366
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	48.3	559	2 B47175	reverse transcript
2	58	48.3	1003	1 GNVWL	HIV-1 retropepsin
3	58	48.3	1003	1 B44001	HIV-1 retropepsin
4	58	48.3	1003	2 T09440	pol polyprotein -
5	58	48.3	1012	1 GNVWL	HIV-1 retropepsin
6	58	48.3	1015	1 GNVWH3	HIV-1 retropepsin
7	54	45.0	276	2 T29689	hypothetical prote
8	52	43.3	1002	1 GNLJND	HIV-1 retropepsin
9	51	42.5	413	2 C91229	hypothetical prote
10	51	42.5	413	2 B86076	hypothetical prote
11	51	42.5	418	2 S40824	hypothetical 48k p
12	51	42.5	424	2 T05785	hypothetical prote
13	50	41.7	567	2 E96764	ethylene-insensiti

14	50	41.7	902	2 T01668	pol polyprotein -
15	50	41.7	1002	2 S54378	pol polyprotein -
16	49	40.8	309	1 B64041	hypothetical prote
17	47.5	39.6	239	2 C84505	hypothetical prote
18	47	39.2	226	2 T20645	reverse transcript
19	47	39.2	559	2 A47175	conserved hypotet
20	47	39.2	747	2 AG3031	hypothetical prote
21	47	39.2	747	2 D8254	pol polyprotein -
22	47	39.2	912	2 S33980	HIV-1 retropepsin
23	47	39.2	1003	1 GNVMA2	hydroxybenzoate oc
24	46.5	38.8	333	2 H82852	large T antigen -
25	46.5	38.8	688	1 TVVPIJ	conserved hypotet
26	46	38.3	392	2 D82330	probable hexosphos
27	46	38.3	456	2 A71501	GlP7/PgP7/UhP7 fam
28	46	38.3	456	2 G81660	transcription fact
29	46	38.3	471	2 T50016	alpha-amylase (EC
30	46	38.3	512	2 S41881	plus fringe glycop
31	46	38.3	823	2 T08092	conserved hypotet
32	45	37.5	130	2 A82599	hypothetical prote
33	45	37.5	144	2 A13330	hypothetical prote
34	45	37.5	334	2 T49195	hexosphosphate tra
35	45	37.5	455	2 F86573	GlP7/PgP7/UhP7 fam
36	45	37.5	455	2 A72050	ethylene-insensiti
37	45	37.5	584	2 B84668	probable two-compo
38	43	37.5	627	2 E55377	pol polyprotein -
39	45	37.5	1009	2 S28061	polyketide synthas
40	45	37.5	2478	2 AH2140	acyl-lacyl-carrier
41	44.5	37.1	385	2 A47245	probable membrane
42	44.5	37.1	633	2 S60408	hypothetical prote
43	44	36.7	121	2 A71031	hypothetical prote
44	44	36.7	401	2 T32167	WFS permease limpo
45	44	36.7	535	2 A82710	

Search completed: March 1, 2004, 19:34:24
Job time : 15.8928 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.30189 Seconds

(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-9148-2

Perfect score: 120

Sequence: 1 YGFKRRQPTWETWTE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	58	48.3	1003	1 POL_HV1H2	P04585 human immun
2	58	48.3	1003	1 POL_HV1Y2	P35963 human immun
3	58	48.3	1007	1 POL_HV1JR	P20875 human immun
4	58	48.3	1015	1 POL_HV1B1	P03366 human immun
5	58	48.3	1015	1 POL_HV1B5	P04587 human immun
6	58	48.3	1015	1 POL_HV1BR	P03367 human immun
7	58	48.3	1015	1 POL_HV1PV	P03368 human immun
8	55	45.8	1006	1 POL_HV1MN	P05961 human immun
9	53	44.2	1002	1 POL_HV1RH	P05959 human immun
10	53	44.2	1003	1 POL_HV1NS	P12437 human immun
11	53	44.2	1003	1 POL_HV1OY	P20892 human immun
12	52	43.3	1002	1 POL_HV1ND	P18802 human immun
13	51	42.5	68	1 ATEB_HIPAM	Q32777 hippopotamu
14	51	42.5	413	1 YIHS_ECOLI	P32140 escherichia
15	50	41.7	567	1 EIL3_ARATH	O23116 arabidopsis
16	50	41.7	1002	1 POL_HV1EL	P04589 human immun
17	50	41.7	1002	1 POL_HV1MA	P04588 human immun

18	50	41.7	1002	1 POL_HV1Z2	P12499 human immun
19	49	40.8	309	1 YBGX_HAEIN	P44298 haemophilus
20	47	39.2	66	1 ATEP_CEREH	Q9mqj9 cervus elap
21	47	39.2	557	1 EIL5_ARATH	Q9fjq5 arabidopsis
22	47	39.2	1003	1 POL_HV1A2	P03369 human immun
23	46.5	38.8	278	1 RCEL_CHRVI	P51762 chromatium
24	46.5	38.8	688	1 TALA_POVIC	P03072 polyomaviru
25	46	38.3	78	1 Y003_BFL2	P42344 bacteriopho
26	46	38.3	456	1 UHPT_CHLMU	Q9PJ38 chlamydia m
27	46	38.3	456	1 UHPT_CHLTR	O84548 chlamydia t
28	46	38.3	471	1 EIL4_ARATH	Q9lx16 arabidopsis
29	45	37.5	149	1 RS19_METKA	Q8twp2 methanopyru
30	45	37.5	435	1 UHPT_CHLPN	Q9z7b9 chlamydia p
31	45	37.5	584	1 EIL1_ARATH	O9slh0 arabidopsis
32	45	37.5	1009	1 POL_SIVGB	P22382 simian immu
33	44.5	37.1	276	1 RCEL_RHOFA	O83005 rhodospseudo
34	44.5	37.1	385	1 STAD_CORSA	P32063 coriandrum
35	44.5	37.1	633	1 GVP3_YEAST	P48566 saccharomyc
36	44	36.7	119	1 YF56_PVRFU	Q8u0r0 pyrococcus
37	44	36.7	121	1 YF39_PVRFU	Q74017 pyrococcus
38	44	36.7	470	1 PROP_CAVPO	O64181 cavia porce
39	44	36.7	518	1 EIL2_ARATH	O23115 arabidopsis
40	44	36.7	628	1 EING_ARATH	O24606 arabidopsis
41	44	36.7	1002	1 POL_HV1U4	P24740 human immun
42	44	36.7	1019	1 POL_SIVS4	P12502 simian immu
43	44	36.7	1022	1 POL_SIVSP	P19505 simian immu
44	44	36.7	1027	1 POL_SIVCZ	P17283 chimpanzee
45	44	36.7	1039	1 M2CI_MOUSE	Q91w89 mus musculu

Search completed: March 1, 2004, 19:24:59

Job time : 9.30189 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:39 ; Search time 33.7076 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-2
Perfect score: 120
Sequence: 1 YGFKRRQPTWETWTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	60	50.0	561	15	Q9DIJ0	human immun
2	58	48.3	212	15	Q9WGU7	human immun
3	58	48.3	237	15	Q9WGU0	human immun
4	58	48.3	237	15	Q9WGU0	human immun
5	58	48.3	237	15	Q9WGU2	human immun
6	58	48.3	237	15	Q9WGU8	human immun
7	58	48.3	237	15	Q9WGU1	human immun
8	58	48.3	433	15	Q79787	human immun
9	58	48.3	523	15	Q9IDB6	human immun
10	58	48.3	523	15	Q9IDB2	human immun
11	58	48.3	523	15	Q9IDB0	human immun
12	58	48.3	524	15	Q9IDB8	human immun
13	58	48.3	545	15	Q9OS14	human immun
14	58	48.3	546	15	Q9OS15	human immun
15	58	48.3	547	15	Q9OS83	human immun
16	58	48.3	547	15	Q9OS82	human immun
17	58	48.3	559	15	Q9URV9	human immun
18	58	48.3	559	15	Q9PXX1	human immun
19	58	48.3	560	15	Q99BA2	human immun
20	58	48.3	560	15	Q99BA1	human immun
21	58	48.3	560	15	Q99BA4	human immun
22	58	48.3	560	15	Q9ORP3	human immun
23	58	48.3	560	15	Q9OEW4	human immun
24	58	48.3	560	15	Q9ORNG	human immun
25	58	48.3	560	15	Q9ORN3	human immun
26	58	48.3	560	15	Q9OEV9	human immun
27	58	48.3	560	15	Q99BA3	human immun
28	58	48.3	560	15	Q9OEW1	human immun
29	58	48.3	560	15	Q99BA5	human immun
30	58	48.3	560	15	Q9ORN4	human immun
31	58	48.3	560	15	Q9ORP4	human immun
32	58	48.3	560	15	Q9ORR8	human immun
33	58	48.3	560	15	Q9ORN5	human immun
34	58	48.3	560	15	Q9ORQ5	human immun
35	58	48.3	560	15	Q9ORP2	human immun
36	58	48.3	560	15	Q9ORR9	human immun
37	58	48.3	560	15	Q99BA9	human immun
38	58	48.3	560	15	Q9OEW2	human immun
39	58	48.3	560	15	Q99BA7	human immun
40	58	48.3	560	15	Q9ORR7	human immun
41	58	48.3	560	15	Q71153	human immun
42	58	48.3	560	15	Q9OEW7	human immun
43	58	48.3	560	15	Q9ORQ6	human immun
44	58	48.3	560	15	Q75395	human immun
45	58	48.3	560	15	Q9ORP5	human immun

Search completed: March 1, 2004, 19:31:50
Job time : 34.7076 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 45.066 Seconds
(without alignments)
106.384 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGFKRQRQTWETWTE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1900s:*

2: geneseqp1900s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	100.0	17	5 ABB77667	Abb77667 Peptide t
2	102.5	90.7	18	5 ABB77666	Abb77666 Peptide t
3	92	81.4	20	5 ABB77679	Abb77679 Generic p
4	90	79.6	19	5 ABB77668	Abb77668 Peptide t
5	90	79.6	19	5 ABB77698	Abb77698 Peptide t
6	90	79.6	19	5 ABB77669	Abb77669 Peptide t
7	79	69.9	21	5 ABB77665	Abb77665 Peptide t
8	73	64.6	11	5 ABB77695	Abb77695 Peptide t
9	73	64.6	12	5 ABB77689	Abb77689 Hydrophob

10	73	64.6	12	5 ABB56174	Abb56174 Cell-targ
11	73	64.6	20	5 ABB77672	Abb77672 Peptide t
12	73	64.6	20	5 ABB77673	Abb77673 Peptide t
13	73	64.6	21	5 ABB77695	Abb77695 Cell pene
14	73	64.6	21	5 ABB77693	Abb77693 Peptide t
15	73	64.6	21	5 ABB77671	Abb77671 Peptide t
16	73	64.6	21	7 ABB68484	Abb68484 Peptide s
17	73	64.6	21	7 ADC22460	Adc22460 Protein-d
18	73	64.6	26	5 ABB56200	Abb56200 Chimeric
19	69	61.1	9	5 ABB77692	Abb77692 Peptide t
20	66.5	58.8	19	5 ABB77670	Abb77670 Peptide t
21	63	55.8	20	5 ABB77694	Abb77694 Peptide t
22	63	55.8	21	5 ABB77674	Abb77674 Peptide t
23	60	53.1	19	5 ABB10106	Abb10106 Peptide t
24	60	53.1	19	5 ABB77699	Abb77699 Peptide t
25	57	50.4	21	5 ABB78716	Abb78716 Peptide p
26	55.5	49.1	19	5 ABB77675	Abb77675 Peptide t
27	55	48.7	21	5 ABB77678	Abb77678 Generic p
28	54	47.8	19	5 ABB77676	Abb77676 Peptide t
29	53.5	47.3	25	5 ABB78714	Abb78714 Retroinhi
30	53	46.9	9	4 ABB23078	Abb23078 HIV All m
31	53	46.9	9	4 ABB19745	Abb19745 HIV A01 m
32	53	46.9	9	4 ABB11817	Abb11817 HIV A01 s
33	53	46.9	9	4 ABB16014	Abb16014 HIV A24 s
34	53	46.9	9	4 ABB16168	Abb16168 HIV A24 s
35	53	46.9	9	4 ABB21039	Abb21039 HIV A03 m
36	53	46.9	9	4 ABB19747	Abb19747 HIV A01 m
37	53	46.9	10	4 ABB18045	Abb18045 HIV B58 s
38	53	46.9	10	5 ABB78711	Abb78711 HIV-1 BH1
39	53	46.9	430	5 ABB47755	Abb47755 Protein #
40	53	46.9	560	4 ABB84201	Abb84201 Amino aci
41	53	46.9	560	6 AAG79973	Aag79973 P2C/C38S/
42	53	46.9	560	7 ADE29023	Ade29023 HIV-1 RT_
43	53	46.9	562	6 ABR44741	Abr44741 Plasmid p
44	53	46.9	562	6 ABR44740	Abr44740 Plasmid p
45	53	46.9	565	6 ABR44743	Abr44743 Plasmid 7

ALIGNMENTS

RESULT 1

ABB77667
ID ABB77667 standard; peptide; 17 AA.

XX	AC	ABB77667;
XX	DT	01-JUL-2002 (first entry)
XX		Peptide transfection agent Pep-1.2.
DE		Peptide transfection agent Pep-1.2.
XX		Intracellular delivery; transfection agent; cancer; infectious disease;
KW		peptide vector.
XX		Synthetic.
OS		WO200210201-A2.
PN		

XX 07-FEB-2002.

XX PD

XX PF 26-JUL-2001; 2001WO-US023406.

XX 31-JUL-2000; 2000US-0221932P.

XX PA (ACTI-) ACTIVE MOTIF.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

XX PI Horndorp K;

XX WPI: 2002-329441/36.

XX

PT Transfection agent that comprises a peptide comprising hydrophobic and

PT hydrophilic domain and having amino acid residues of specified length is

PT useful for a non-covalent association with and transport of a

PT heterologous compound into a cell.

XX

PS Claim 12; Page 16; 156pp; English.

XX

CC The invention relates to a transfection agent comprises a peptide of

CC about 16 - 30 amino acids in length. Peptides of the invention comprise a

CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

CC between the domains and a functional group conjugated to at least one

CC terminal of the peptide. Peptides of the invention are useful for a non-

CC covalent association with and transport of a heterologous compound into a

CC cell. They are also useful for promoting the cellular internalisation of

CC at least one member e.g. peptide, proteins, antibodies, their derivatives

CC and/or conjugates. They may form part of a pharmaceutical composition to

CC deliver the compound selected from a diagnostic or therapeutic compound,

CC to treat at least one condition such as cancer or an infectious disease,

CC or which targets a cancerous cell or pathogen-infected cell and to

CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.

CC The agent of the invention has a transfection efficiency of at least 5%

CC for at least two of the members of the group of the compounds. The agent

CC has a good delivery efficiency for a broad spectrum of compounds and cell

CC types, has a low toxicity, are easy to handle and easy to formulate in

CC conjunction with the many different compound types that it can deliver.

CC The peptides are serum sensitive, thus they bode particularly well for

CC systemic and/or localised in patients. The current sequence represents

CC the peptide transfection agent Pep-1.1

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 113; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGFKRRQQTWETWTE 17

|||||

Db 1 YGFKRRQQTWETWTE 17

Search completed: March 1, 2004, 16:55:40

Job time : 46.066 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 11.1462 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGFKRRQQTWETWTE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	53	46.9	559	2	B47175	reverse transcriptase	
2	53	46.9	1003	1	GNWMLV	HIV-1 retropepsin	
3	53	46.9	1003	1	B44001	HIV-1 retropepsin	
4	53	46.9	1003	2	T09440	pol polyprotein -	
5	53	46.9	1012	1	GNWVWL	HIV-1 retropepsin	
6	53	46.9	1015	1	GNVWH3	HIV-1 retropepsin	
7	50	44.2	276	2	T29689	hypothetical prote	
8	50	44.2	413	2	C91229	hypothetical prote	
9	50	44.2	413	2	B6076	hypothetical prote	
10	50	44.2	418	2	S40524	hypothetical 48K p	
11	50	44.2	424	2	T05785	hypothetical prote	
12	49	43.4	487	4	S51886	hypothetical prote	
13	49	43.4	492	2	S51885	probable membrane	

14 49 43.4 528 4 S51887
15 48.5 42.9 859 1 VCLJ83
16 48 42.5 268 2 B87676
17 48 42.5 455 2 F86573
18 48 42.5 455 2 A72050
19 48 42.5 456 2 A71501
20 48 42.5 456 2 G81660
21 48 42.5 902 2 T01668
22 48 42.5 1002 2 S54378
23 47 41.6 229 2 T06346
24 47 41.6 431 2 AH2006
25 47 41.6 633 2 S60408
26 47 41.6 1002 1 GNJND
27 46.5 41.2 1768 2 E85062
28 46 40.7 269 2 F85946
29 46 40.7 502 2 T41341
30 46 40.7 823 2 T06092
31 46 40.7 1103 2 T42022
32 46 40.7 1171 2 T00380
33 45.5 40.3 836 2 T31613
34 45 39.8 130 2 A82599
35 45 39.8 238 2 S73123
36 45 39.8 298 2 B71872
37 45 39.8 334 2 T49195
38 45 39.8 531 2 T50964
39 45 39.8 621 2 H84922
40 45 39.8 689 2 T35882
41 45 39.8 2212 2 T28157
42 45 39.8 2647 2 T28161
43 44.5 39.4 121 2 A71031
44 44.5 39.4 239 2 C84505
45 44.5 39.4 511 2 T48777

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 16:39:39 ; Search time 6.89623 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGFKKRRQTWETWTE I7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	46.9	1003	1	POL_HVIH2
2	53	46.9	1003	1	POL_HVIY2
3	53	46.9	1006	1	POL_HVIMN
4	53	46.9	1007	1	POL_HVILJR
5	53	46.9	1015	1	POL_HVILB1
6	53	46.9	1015	1	POL_HVILB5
7	53	46.9	1015	1	POL_HVILBR
8	53	46.9	1015	1	POL_HVILPV
9	50	44.2	413	1	YIHS_ECOLI
10	48.5	42.9	859	1	ENV_EIAV3
11	48	42.5	456	1	UHPT_CHLPN
12	48	42.5	456	1	UHPT_CHLMU
13	48	42.5	456	1	UHPT_CHLTR
14	48	42.5	1002	1	POL_HVIEL
15	48	42.5	1002	1	POL_HVIMA
16	48	42.5	1002	1	POL_HVIRH
17	48	42.5	1002	1	POL_HVIZ2
					P04585 human immun
					P35963 human immun
					P05961 human immun
					P20875 human immun
					P03366 human immun
					P04587 human immun
					P03367 human immun
					P03368 human immun
					P32140 escherichia
					P22429 equine infe
					Q927n9 chlamydia p
					Q9pj18 chlamydia m
					O84548 chlamydia t
					P04589 human immun
					P04588 human immun
					P05959 human immun
					P12499 human immun

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 16:40:39 ; Search time 31.8349 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-3
Perfect score: 113
Sequence: 1 YGFKRRQIWTWTE 17
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp Vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

18	48	42.5	1003	1	POL_HVIN5	P12497 human immun
19	48	42.5	1003	1	POL_HVIOY	P20892 human immun
20	47	41.6	229	1	CEN4_SOYBN	P49160 glycine max
21	47	41.6	633	1	GIP3_YEAST	P48566 saccharomyc
22	47	41.6	1002	1	POL_HVIND	P18802 human immun
23	46	40.7	78	1	YOO9_BPL2	P42544 bacterioph
24	46	40.7	229	1	CEN4_SPTOL	Q9m314 spinacia ol
25	46	40.7	1103	1	CHS6_USTMA	O13395 ustilago ma
26	46	40.7	1171	1	ZBE4_HUMAN	O75132 homo sapien
27	45	39.8	238	1	YCS3_PORPU	P51202 porphyra pu
28	44.5	39.4	119	1	YF56_PYRHO	Q8u0n0 pyrococcus
29	44.5	39.4	121	1	YF39_PYRHO	O74017 pyrococcus
30	44.5	39.4	859	1	ENV_EIAV1	P22427 equine infe
31	44.5	39.4	859	1	ENV_EIAV2	P22428 equine infe
32	44.5	39.4	859	1	ENV_EIAV9	P11306 equine infe
33	44.5	39.4	859	1	ENV_EIAVC	P32541 equine infe
34	44.5	39.4	859	1	ENV_EIAW	P16082 equine infe
35	44.5	39.4	859	1	ENV_EIAV	P06751 equine infe
36	44.5	39.4	860	1	ENV_EIAV5	P22430 equine infe
37	44	38.9	280	1	RIP1_HORVU	P22444 hordeum vul
38	44	38.9	280	1	RIP2_HORVU	P04399 hordeum vul
39	44	38.9	612	1	OTC_BOVIN	O19094 bos taurus
40	44	38.9	1019	1	POL_SIVS4	P12502 simian immu
41	44	38.9	1022	1	POL_SIVSP	P19305 simian immu
42	44	38.9	1054	1	POL_SIVPK	P05897 simian immu
43	44	38.9	1056	1	POL_SIVM1	P05896 simian immu
44	43.5	38.5	472	1	EIBL_ADE51	P10546 human adeno
45	43	38.1	344	1	RHAT_ECOLI	P27125 escherichia

Search completed: March 1, 2004, 19:25:00
Job time : 7.89623 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Q91dj7 human immun
Q91ax3 human immun
Q91des human immun
Q91df6 human immun
Q90s63 human immun
Q90s45 human immun
Q90s47 human immun
Q88988 human immun
Q8875 human immun
Q88687 human immun
Q91m29 human immun
Q7av29 human immun
Q9wgu7 human immun
Q988v3 human immun
Q9wgv0 human immun
Q9wgv3 human immun
Q9wgv7 human immun
Q9wgv4 human immun
Q9wgv5 human immun
Q9wgv9 human immun
Q9w8h5 human immun
Q9w9u0 human immun
Q9wgv6 human immun
Q9wgv7 human immun
Q9wgv2 human immun
Q9wgv5 human immun
Q9wgv1 human immun
Q9wgv2 human immun
Q9wgv6 human immun
Q9wgv8 human immun
Q9wgv3 human immun
Q9wgv4 human immun
Q9wgv1 human immun
Q9wgv4 human immun
Q9787 human immun
Q9dlj8 human immun
Q9ldi3 human immun
Q9ldi9 human immun
Q9ldc7 human immun
Q9ldb6 human immun
Q9ldb2 human immun
Q9ldf2 human immun

56.5 50.0 524 15 Q91DJ7
56.5 50.0 1009 15 Q8JX3
55.5 49.1 524 15 Q91DE9
55.5 49.1 524 15 Q91DF8
55.5 49.1 560 15 Q90S63
55.5 49.1 560 15 Q90S45
55.5 49.1 560 15 Q90S47
55.5 49.1 582 15 Q8Q988
55.5 49.1 588 15 Q8Q875
55.5 49.1 593 15 Q8Q867
55.5 49.1 1002 15 Q91M29
55.5 49.1 1434 15 Q7SV29
53 46.9 212 15 Q9WGU7
53 46.9 225 15 Q988V3
53 46.9 237 15 Q9WGV0
53 46.9 237 15 Q9WGV3
53 46.9 237 15 Q9WGV7
53 46.9 237 15 Q9WGV4
53 46.9 237 15 Q9WGV5
53 46.9 237 15 Q9WGV9
53 46.9 237 15 Q9W8H5
53 46.9 237 15 Q9W9U0
53 46.9 237 15 Q9WGV6
53 46.9 237 15 Q9WGV7
53 46.9 237 15 Q9WGV2
53 46.9 237 15 Q9WGV5
53 46.9 237 15 Q9WGV1
53 46.9 237 15 Q9WGV2
53 46.9 237 15 Q9WGV3
53 46.9 237 15 Q9WGV4
53 46.9 237 15 Q9WGV1
53 46.9 237 15 Q9WGV4
53 46.9 433 15 Q9787
53 46.9 514 15 Q9DLJ8
53 46.9 519 15 Q9IDL3
53 46.9 523 15 Q9IDL9
53 46.9 523 15 Q9IDC7
53 46.9 523 15 Q9IDB6
53 46.9 523 15 Q9IDB2
53 46.9 523 15 Q9IDF2

Search completed: March 1, 2004, 19:31:51
Job time : 32.8349 secs

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGFKFKRKPWTWETWTE 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	19	5	ABB77668
2	132	100.0	19	5	ABB77668 Peptide t
3	132	100.0	19	5	ABB77669
4	122	92.4	20	5	ABB77679
5	97.5	73.9	18	5	ABB77666
6	90	68.2	17	5	ABB77667
7	75	56.8	21	5	ABB77665
8	69	52.3	9	5	ABB77692
9	69	52.3	11	5	ABB77695

XX PD 07-FEB-2002.

XX PD 26-JUL-2001; 2001WO-US023406.

XX PF 31-JUL-2000; 2000US-0221932P.

XX PR (ACTI-) ACTIVE MOTIF.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

XX PI Hornodorp K;

XX DR WPI; 2002-329441/36.

XX PT Transfection agent that comprises a peptide comprising hydrophobic and

XX PT hydrophilic domain and having amino acid residues of specified length is

PT useful for a non-covalent association with and transport of a

XX PT heterologous compound into a cell.

XX PS Claim 12; Page 16; 156pp; English.

XX CC The invention relates to a transfection agent comprises a peptide of

CC about 16 - 30 amino acids in length. Peptides of the invention comprise a

CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

CC between the domains and a functional group conjugated to at least one

CC terminal of the peptide. Peptides of the invention are useful for a non-

CC covalent association with and transport of a heterologous compound into a

CC cell. They are also useful for promoting the cellular internalisation of

CC at least one member e.g. peptide, proteins, antibodies, their derivatives

CC and/or conjugates. They may form part of a pharmaceutical composition to

CC deliver the compound selected from a diagnostic or therapeutic compound,

CC to treat at least one condition such as cancer or an infectious disease,

CC or which targets a cancerous cell or pathogen-infected cell and to

CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.

CC The agent of the invention has a transfection efficiency of at least 5%.

CC for at least two of the members of the group of the compounds. The agent

CC has a good delivery efficiency for a broad spectrum of compounds and cell

CC types, has a low toxicity, are easy to handle and easy to formulate in

CC conjunction with the many different compound types that it can deliver.

CC The peptides are serum sensitive, thus they bind particularly well for

CC systemic and/or localised in patients. The current sequence represents

CC the peptide transfection agent pep-3

RESULT 1
ABB77668
ID ABB77668 standard: peptide: 19 AA.

```

Query Match      100.0%; Score 132; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YGFKKFRKWTWMTWMT 19
        ||| ||||| ||||| |||
Db       1 YGFKKFRKWTWMTWMT 19

RESULT 2
ASB77698

```

ID	ABB77698 standard; peptide; 19 Aa.
XX	ABB77698;
AC	ABB77698;
XX	XX
DT	01-JUL-2002 (first entry)
XX	XX
DE	Peptide transfection agent Pep-4.1-Cya.
XX	XX
XX	Intracellular delivery; transfection agent; cancer; infectious disease;
KW	peptide vector.
XX	XX
OS	Synthetic.
XX	XX
PN	W0200210201-A2.
PN	XX
PD	07-FEB-2002.
PD	XX
PF	26-JUL-2001; 2001WO-US023406.
XX	XX
XX	31-JUL-2000; 2000US-0221932P.
PR	{ACTI-} ACTIVE MOTIF.
PA	(CNRS) CENT NAT RECH SCI.
PA	XX
PI	Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI	Hornadorp K;
DR	XX
XX	WPI; 2002-329441/36.
XX	XX
PT	Transfection agent that comprises a peptide comprising hydrophobic and
PT	hydrophilic domain and having amino acid residues of specified length is
PT	useful for a non-covalent association with and transport of a
PT	heterologous compound into a cell.
PT	XX
PS	Example 4; Page 77; 156pp; English.
XX	XX
CC	The invention relates to a transfection agent comprises a peptide of
CC	about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC	hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC	between the domains and a functional group conjugated to at least one
CC	terminal of the peptide. Peptides of the invention are useful for a non-
CC	covalent association with and transport of a heterologous compound into a
CC	cell. They are also useful for promoting the cellular internalisation of
CC	at least one member e.g. peptide, proteins, antibodies, their derivatives
CC	and/or conjugates. They may form part of a pharmaceutical composition to
CC	deliver the compound selected from a diagnostic or therapeutic compound,
CC	to treat at least one condition such as cancer or an infectious disease,
CC	or which targets a cancerous cell or pathogen-infected cell and to
CC	deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC	The agent of the invention has a transfection efficiency of at least 5%
CC	for at least two of the members of the group of the compounds. The agent
CC	has a good delivery efficiency for a broad spectrum of compounds and cell
CC	types, has a low toxicity, are easy to handle and easy to formulate in
CC	conjunction with the many different compound types that it can deliver.
CC	The peptides are serum sensitive, thus they bode particularly well for
CC	systemic and/or localised in patients. The current sequence represents
CC	the peptide transfection agent Pep-4.1-Cya

CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent Pep-2.6
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 132; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGPKFKRKPTWTWETWTE 19
|||||
DB 1 YGPKFKRKPTWTWETWTE 19

Search completed: March 1, 2004, 16:55:52
Job time : 62.3679 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGPKFKRKPTWTWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	%	Match	Length	DB	ID	Description
1	54	40.9	332	2	E69312				nitrate reductase
2	54	40.9	1003	1	GNWVLV				HIV-1 retropepsin
3	54	40.9	1003	1	B44001				HIV-1 retropepsin
4	54	40.9	1003	2	T09440				pol polyprotein -
5	54	40.9	1012	1	GNWVWL				HIV-1 retropepsin
6	54	40.9	1015	1	GNVWH3				HIV-1 retropepsin
7	53	40.2	392	2	G82746				hypothetical prote
8	53	40.2	559	2	B47175				reverse transcript
9	52	39.4	667	1	VCLJGL				env polyprotein pr
10	52	39.4	814	2	A95206				glycosyl transfera
11	52	39.4	902	2	T01668				pol polyprotein -
12	52	39.4	1002	2	S54378				pol polyprotein -
13	51.5	39.0	1780	2	A85045				probable glucan sy

14 50 37.9 130 2 A32599 conserved hypothet
15 49.5 37.5 148 2 S46515 purolindoline-a pre
16 49.5 37.5 222 2 A68102 protein W09G10.1 l
17 48.5 36.7 223 2 A29770 cerebellar degener
18 48.5 36.7 660 2 E81839 probable transmem
19 48.5 36.7 675 2 E81101 transporter, BCC1
20 48.5 36.7 1103 2 T42022 probable chitin sy
21 48 36.4 1002 1 GNLJND HIV-1 retropepsin
22 47.5 36.0 625 2 T6184 sucrose-fructan 6-
23 47 35.6 86 2 T05982 hypothetical prote
24 47 35.6 198 2 G72489 hypothetical prote
25 47 35.6 227 2 AC0944 conserved hypothet
26 47 35.6 341 2 A83644 hypothetical prote
27 47 35.6 413 2 C91229 hypothetical prote
28 47 35.6 413 2 B86076 hypothetical prote
29 47 35.6 418 2 S40854 hypothetical 48K p
30 47 35.6 445 2 A41621 env polyprotein M
31 47 35.6 477 2 S42162 sucrose hydrolase
32 47 35.6 477 2 C91034 sucrose-6 phosphat
33 47 35.6 477 2 D65878 Spot 3 protein and
34 47 35.6 623 2 T47542 vacuolar sorting r
35 47 35.6 628 2 T02602 probable vacuolar
36 47 35.6 628 2 T02604 gamma-aminobutyric
37 46.5 35.2 598 2 I51368 hypothetical prote
38 46.5 35.2 794 2 S50687 protein T05A8.2 (i
39 46 34.8 221 2 F88082 hypothetical prote
40 46 34.8 262 2 F82519 dihydrogenase DtlA,
41 46 34.8 469 2 T50934 vacuolar sorting r
42 46 34.8 624 2 T00044 probable vacuolar
43 46 34.8 625 2 F84706 cytochrome c-type
44 46 34.8 643 2 AG0787 cytochrome c-type
45 46 34.8 643 2 AH0960

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-4
Perfect score: 132
Sequence: 1 YGFKFKFQWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: March 1, 2004, 19:34:28

Job time : 15.5485 secs

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	43.2	1006	1	POL_HVIMN
2	55	41.7	789	1	LF1B_DROME
3	54	40.9	332	1	HMEC_ARCFU
4	54	40.9	1003	1	POL_HV1H2
5	54	40.9	1003	1	POL_HV1Y2
6	54	40.9	1007	1	POL_HV1JR
7	54	40.9	1015	1	POL_HV1B1
8	54	40.9	1015	1	POL_HV1B5
9	54	40.9	1015	1	POL_HV1BR
10	54	40.9	1015	1	POL_HV1PV
11	52	39.4	667	1	ENV_GALV
12	52	39.4	1002	1	POL_HV1EL
13	52	39.4	1002	1	POL_HV1MA
14	52	39.4	1002	1	POL_HV1Z2
15	50	37.9	789	1	LF1A_DROME
16	49.5	37.5	148	1	PU1A_WHEAT
17	49	37.1	856	1	ENV_HV2NZ
					P05961 human immun
					P11956 drosophila
					O29749 archaeoglob
					P04585 human immun
					P35963 human immun
					P20875 human immun
					P03366 human immun
					P04587 human immun
					P03367 human immun
					P21415 gibbon ape
					P04589 human immun
					P04588 human immun
					P12499 human immun
					P11995 drosophila
					P33432 triticum ae
					P05863 human immun

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OM protein - protein search, using sw model
Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

P05959 human immun
P12497 human immun
P20892 human immun
P51861 homo sapien
O13395 ustilago na
O70146 mus musculu
P18802 human immun
P43022 salmonella
Q15777 homo sapien
P32140 escherichia
P40714 escherichia
P39961 saccharomyc
P42544 bacterioph
Q9cle3 sus scrofa
P24105 human immun
P15831 human immun
P24740 human immun
P17283 chimpanzee
P51973 neisseria g
P54942 bacillus su
P75083 mycoplasma
Q21693 caenorhabdi
P43236 oryctolagus
P27125 escherichia
Q8r0f3 mus musculu
Q8rbk3 homo sapien
O74794 schizosacch
Q10660 caenorhabdi

18 49 37.1 1002 1 POL_HVIRH
19 49 37.1 1003 1 POL_HVINS
20 49 37.1 1003 1 POL_HVIOY
21 48.5 36.7 223 1 CDR1_HUMAN
22 48.5 36.7 1103 1 CHS6_USMA
23 48 36.4 627 1 TES1_MOUSE
24 48 36.4 1002 1 POL_HVIND
25 47 33.6 227 1 YIIY_SALTY
26 47 35.6 294 1 239F_HUMAN
27 47 35.6 413 1 YIHS_ECOLI
28 47 35.6 477 1 CSCA_ECOLI
29 46.5 35.2 794 1 YE14_YEAST
30 46 34.8 78 1 Y009_BPL2
31 46 34.8 330 1 CATK_PIG
32 46 34.8 859 1 ENV_HV2CA
33 46 34.8 859 1 ENV_HV2D2
34 46 34.8 1002 1 POL_HV104
35 46 34.8 1027 1 POL_SIVCZ
36 45.5 34.5 691 1 CONA_NEIGO
37 45 34.1 132 1 YXEC_BAGSU
38 45 34.1 203 1 Y028_MYCPN
39 45 34.1 228 1 IFE2_CAEEL
40 45 34.1 329 1 CATK_RABIT
41 45 34.1 344 1 RHAT_ECOLI
42 45 34.1 372 1 SUM1_MOUSE
43 45 34.1 374 1 SUM1_HUMAN
44 45 34.1 377 1 CCHL_SCHPO
45 45 34.1 393 1 DOM3_CAEEL

Search completed: March 1, 2004, 19:25:01
Job time : 8.70755 secs

Title: US-09-915-91AB-4
Perfect score: 132
Sequence: 1 YGFKKFKPWTWETWTE 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1 60 45.5 560 15 Q90RR5 Q90rr-5 human immun
2 60 45.5 560 15 Q90RR6 Q90rr-6 human immun
3 60 45.5 560 15 Q90RR4 Q90rr-4 human immun
4 58 43.9 1033 15 Q79666 Q79666 human immun
5 57 43.2 225 15 Q998V3 Q998v3 human immun
6 57 43.2 237 15 Q9WGV3 Q9wgv3 human immun
7 57 43.2 237 15 Q9WGV7 Q9wgv7 human immun
8 57 43.2 237 15 Q9WGV5 Q9wgv5 human immun
9 57 43.2 237 15 Q9WGV0 Q9wgv0 human immun
10 57 43.2 237 15 Q9WGV5 Q9wgv5 human immun
11 57 43.2 237 15 Q9WGV9 Q9wgv9 human immun
12 57 43.2 237 15 Q9W8H5 Q9w8h5 human immun
13 57 43.2 237 15 Q9WGX6 Q9wgx6 human immun
14 57 43.2 237 15 Q9WGX6 Q9wgx6 human immun
15 57 43.2 237 15 Q9WGX5 Q9wgx5 human immun
16 57 43.2 237 15 Q9WGX6 Q9wgx6 human immun
17 57 43.2 237 15 Q9WGV6 Q9wgv6 human immun
18 57 43.2 237 15 Q9WGV8 Q9wgv8 human immun
19 57 43.2 237 15 Q9WGV3 Q9wgv3 human immun
20 57 43.2 237 15 Q9WGW4 Q9wgw4 human immun
21 57 43.2 237 15 Q9WGV4 Q9wgv4 human immun
22 57 43.2 519 15 Q91DI3 Q9idi3 human immun
23 57 43.2 523 15 Q91DI9 Q9idi9 human immun
24 57 43.2 523 15 Q91DC7 Q9ide7 human immun
25 57 43.2 523 15 Q91DF2 Q9idf2 human immun
26 57 43.2 524 15 Q91DI8 Q9idi8 human immun
27 57 43.2 524 15 Q91DI7 Q9idi7 human immun
28 57 43.2 524 15 Q91DE9 Q9ide9 human immun
29 57 43.2 524 15 Q91DD1 Q9idd1 human immun
30 57 43.2 524 15 Q91DI6 Q9idi6 human immun
31 57 43.2 524 15 Q91DF8 Q9idf8 human immun
32 57 43.2 524 15 Q91DI2 Q9idi2 human immun
33 57 43.2 524 15 Q91DI4 Q9idi4 human immun
34 57 43.2 524 15 Q91DI5 Q9idi5 human immun
35 57 43.2 524 15 Q91DD2 Q9idd2 human immun
36 57 43.2 547 15 Q90S79 Q9os79 human immun
37 57 43.2 547 15 Q90S76 Q9os76 human immun
38 57 43.2 547 15 Q90S80 Q9os80 human immun
39 57 43.2 547 15 Q90S77 Q9os77 human immun
40 57 43.2 547 15 Q90S81 Q9os81 human immun
41 57 43.2 547 15 Q90S78 Q9os78 human immun
42 57 43.2 560 15 Q90RS2 Q9ors2 human immun
43 57 43.2 560 15 Q90RP0 Q9orpo human immun
44 57 43.2 560 15 Q99BA6 Q99ba6 human immun
45 57 43.2 560 15 Q71157 Q71157 human immun

Search completed: March 1, 2004, 13:31:52
Job time : 36.5802 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKFKRPWTWETWTE 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	19	5	ABB77668
2	132	100.0	19	5	ABB77668 Peptide t
3	132	100.0	19	5	ABB77669
4	122	92.4	20	5	ABB77679
5	97.5	73.9	18	5	ABB77666
6	90	68.2	17	5	ABB77667
7	75	56.8	21	5	ABB77665
8	69	52.3	9	5	ABB77692
9	69	52.3	11	5	ABB77695

10 69 52.3 12 5 ABB77689 ABB77689 Hydrophob
11 69 52.3 12 5 ABB76174 ABB76174 Cell-targ
12 69 52.3 19 5 ABB77670 ABB77670 Peptide t
13 69 52.3 20 5 ABB77672 ABB77672 Peptide t
14 69 52.3 20 5 ABB77673 ABB77673 Peptide t
15 69 52.3 21 5 ABB77695 ABB77695 Cell pene
16 69 52.3 21 5 ABB77693 ABB77693 Peptide t
17 69 52.3 21 5 ABB77671 ABB77671 Peptide t
18 69 52.3 21 5 ABB77674 ABB77674 Peptide t
19 69 52.3 21 7 ABB77674 ABB77674 Peptide s
20 69 52.3 21 7 ABB77674 ABB77674 Peptide s
21 69 52.3 21 7 ABB77674 ABB77674 Peptide s
22 69 52.3 21 7 ABB77674 ABB77674 Peptide s
23 69 52.3 21 7 ABB77674 ABB77674 Peptide s
24 69 52.3 21 7 ABB77674 ABB77674 Peptide s
25 69 52.3 21 7 ABB77674 ABB77674 Peptide s
26 69 52.3 21 7 ABB77674 ABB77674 Peptide s
27 69 52.3 21 7 ABB77674 ABB77674 Peptide s
28 69 52.3 21 7 ABB77674 ABB77674 Peptide s
29 69 52.3 21 7 ABB77674 ABB77674 Peptide s
30 69 52.3 21 7 ABB77674 ABB77674 Peptide s
31 69 52.3 21 7 ABB77674 ABB77674 Peptide s
32 69 52.3 21 7 ABB77674 ABB77674 Peptide s
33 69 52.3 21 7 ABB77674 ABB77674 Peptide s
34 69 52.3 21 7 ABB77674 ABB77674 Peptide s
35 69 52.3 21 7 ABB77674 ABB77674 Peptide s
36 69 52.3 21 7 ABB77674 ABB77674 Peptide s
37 69 52.3 21 7 ABB77674 ABB77674 Peptide s
38 69 52.3 21 7 ABB77674 ABB77674 Peptide s
39 69 52.3 21 7 ABB77674 ABB77674 Peptide s
40 69 52.3 21 7 ABB77674 ABB77674 Peptide s
41 69 52.3 21 7 ABB77674 ABB77674 Peptide s
42 69 52.3 21 7 ABB77674 ABB77674 Peptide s
43 69 52.3 21 7 ABB77674 ABB77674 Peptide s
44 69 52.3 21 7 ABB77674 ABB77674 Peptide s
45 69 52.3 21 7 ABB77674 ABB77674 Peptide s

ALIGNMENTS

RESULT 1
ID ABB77668 standard; peptide; 19 AA.
XX
AC ABB77668;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-3.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.

XX
PD 07-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-US023406.
XX
PR 31-JUL-2000; 2000US-0221932P.
XX
PA (ACTI-) ACTIVE MOTIF.
XX (CNRS) CENT NAT RECH SCI.
XX
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
XX Horndorp K;
XX WPI; 2002-329441/36.
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
XX hydrophilic domain and having amino acid residues of specified length is
XX useful for a non-covalent association with and transport of a
XX heterologous compound into a cell.
XX
XX Claim 12; Page 16; 156pp; English.
XX
XX The invention relates to a transfection agent comprising a peptide of
XX about 16 - 30 amino acids in length. Peptides of the invention comprise a
XX hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
XX between the domains and a functional group conjugated to at least one
XX terminal of the peptide. Peptides of the invention are useful for a non-
XX covalent association with and transport of a heterologous compound into a
XX cell. They are also useful for promoting the cellular internalisation of
XX at least one member e.g. peptide, proteins, antibodies, their derivatives
XX and/or conjugates. They may form part of a pharmaceutical composition to
XX deliver the compound selected from a diagnostic or therapeutic compound,
XX to treat at least one condition such as cancer or an infectious disease,
XX or which targets a cancerous cell or pathogen-infected cell and to
XX deliver a peptide or inhibitor that disrupts the activity of the enzyme.
XX The agent of the invention has a transfection efficiency of at least 5%
XX for at least two of the members of the group of the compounds. The agent
XX has a good delivery efficiency for a broad spectrum of compounds and cell
XX types, has a low toxicity, are easy to handle and easy to formulate in
XX conjunction with the many different compound types that it can deliver.
XX The peptides are serum sensitive, thus they are particularly well for
XX systemic and/or localised in patients. The current sequence represents
XX the peptide transfection agent Pep-3
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 132; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGFKKRPKPTWWTWTE 19
Db 1 YGFKKRPKPTWWTWTE 19

RESULT 2
ABB77698

ID ABB77698 standard; peptide; 19 AA.

XX AC ABB77698;

XX DT 01-JUL-2002 (first entry)

XX DE Peptide transfection agent Pep-4.1-Cya.

XX KW Intracellular delivery; transfection agent; cancer; infectious disease;

XX KW peptide vector.

XX OS Synthetic.

XX PN W0200210201-A2.

XX PD 07-FEB-2002.

XX PF 26-JUL-2001; 2001WO-US023406.

XX PR 31-JUL-2000; 2000US-0221932P.

XX PA (ACTI-) ACTIVE MOTIF.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

XX PI Horndorp K;

XX DR WPI; 2002-329441/36.

XX PT Transfection agent that comprises a peptide comprising hydrophobic and

XX PT hydrophilic domain and having amino acid residues of specified length is

XX PT useful for a non-covalent association with and transport of a

XX PT heterologous compound into a cell.

XX PS Example 4; Page 77; 156pp; English.

XX CC The invention relates to a transfection agent comprises a peptide of

XX CC about 16 - 30 amino acids in length. Peptides of the invention comprise a

XX CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

XX CC between the domains and a functional group conjugated to at least one

XX CC terminal of the peptide. Peptides of the invention are useful for a non-

XX CC covalent association with and transport of a heterologous compound into a

XX CC cell. They are also useful for promoting the cellular internalisation of

XX CC at least one member e.g. peptide, proteins, antibodies, their derivatives

XX CC and/or conjugates. They may form part of a pharmaceutical composition to

XX CC deliver the compound selected from a diagnostic or therapeutic compound,

XX CC to treat at least one condition such as cancer or an infectious disease,

XX CC or which targets a cancerous cell or pathogen-infected cell and to

XX CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.

XX CC The agent of the invention has a transfection efficiency of at least 5%

XX CC for at least two of the members of the group of the compounds. The agent

XX CC has a good delivery efficiency for a broad spectrum of compounds and cell

XX CC types, has a low toxicity, are easy to handle and easy to formulate in

XX CC conjunction with the many different compound types that it can deliver.

XX CC The peptides are serum sensitive, thus they bode particularly well for

XX CC systemic and/or localised in patients. The current sequence represents

XX CC the peptide transfection agent Pep-4.1-Cya

XX SQ Sequence 19 AA;

XX Query Match 100.0%; Score 132; DB 5; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 5.8e-11;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Caps 0;

XX QY 1 YGFKKFRKPTWWTWTE 19

XX DB 1 YGFKKFRKPTWWTWTE 19

XX RESULT 3

XX ABB77669

XX ID ABB77669 standard; peptide; 19 AA.

XX AC ABB77669;

XX DT 01-JUL-2002 (first entry)

XX DE Peptide transfection agent Pep-2.6.

XX KW Intracellular delivery; transfection agent; cancer; infectious disease;

XX KW peptide vector.

XX OS Synthetic.

XX PN W0200210201-A2.

XX PD 07-FEB-2002.

XX PF 26-JUL-2001; 2001WO-US023406.

XX PR 31-JUL-2000; 2000US-0221932P.

XX PA (ACTI-) ACTIVE MOTIF.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;

XX PI Horndorp K;

XX DR WPI; 2002-329441/36.

XX PT Transfection agent that comprises a peptide comprising hydrophobic and

XX PT hydrophilic domain and having amino acid residues of specified length is

XX PT useful for a non-covalent association with and transport of a

XX PT heterologous compound into a cell.

XX PS Claim 12; Page 16; 156pp; English.

XX CC The invention relates to a transfection agent comprises a peptide of

XX CC about 16 - 30 amino acids in length. Peptides of the invention comprise a

XX CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence

XX CC between the domains and a functional group conjugated to at least one

XX CC terminal of the peptide. Peptides of the invention are useful for a non-

XX CC covalent association with and transport of a heterologous compound into a

XX CC cell. They are also useful for promoting the cellular internalisation of

XX CC at least one member e.g. peptide, proteins, antibodies, their derivatives

XX CC and/or conjugates. They may form part of a pharmaceutical composition to

XX CC deliver the compound selected from a diagnostic or therapeutic compound,

XX CC to treat at least one condition such as cancer or an infectious disease,

XX CC or which targets a cancerous cell or pathogen-infected cell and to

XX CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.

XX CC The agent of the invention has a transfection efficiency of at least 5%

XX CC for at least two of the members of the group of the compounds. The agent

XX CC has a good delivery efficiency for a broad spectrum of compounds and cell

XX CC types, has a low toxicity, are easy to handle and easy to formulate in

XX CC conjunction with the many different compound types that it can deliver.

XX CC The peptides are serum sensitive, thus they bode particularly well for

XX CC systemic and/or localised in patients. The current sequence represents

XX CC the peptide transfection agent Pep-2.6

CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 3%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
CC the peptide transfection agent pep-2.6
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 132; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e-11; Mismatches 0; Gaps 0;
Matches 19; Conservative 0; Indels 0;

QY 1 YGFKFKRPWTWETWTE 19
| | | | | | | | | | | | | | | | | | | | |
DB 1 YGFKFKRPWTWETWTE 19

Search completed: March 1, 2004, 16:55:52
Job time : 50.3679 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKFKRPWTWETWTE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	40.9	332	2 E69312	nitrate reductase
2	54	40.9	1003	1 GNWMLV	HIV-1 retropepsin
3	54	40.9	1003	1 B44001	HIV-1 retropepsin
4	54	40.9	1003	2 T09440	pol polyprotein -
5	54	40.9	1012	1 GNWVWL	HIV-1 retropepsin
6	54	40.9	1015	1 GNWVH3	HIV-1 retropepsin
7	53	40.2	392	2 G82746	hypothetical prote
8	53	40.2	559	2 B47175	reverse transcript
9	52	39.4	667	1 VCLJGL	env polyprotein pr
10	52	39.4	814	2 A95206	glycosyl transfera
11	52	39.4	902	2 T01668	pol polyprotein -
12	52	39.4	1002	2 S54378	pol polyprotein -
13	51.5	39.0	1780	2 A85045	probable glucan sy

14 50 37.9 130 2 A82599 conserved hypothet
15 49.5 37.5 146 2 S46S15 purioindoline-a pre
16 49.5 37.5 222 2 A88102 Protein W09010.1 f
17 48.5 36.7 223 2 A29770 cerebellar degener
18 48.5 36.7 660 2 E81839 probable transmem
19 48.5 36.7 675 2 E81101 transporter, BCCP
20 48.5 36.7 T42022 Probable chitin sy
21 48 36.4 1002 1 GNLJND HIV-1 retropepsin
22 47.5 36.0 625 2 T06184 sucrose-fructan 6-
23 47 35.6 86 2 T05982 hypothetical prote
24 47 35.6 198 2 G72489 hypothetical prote
25 47 35.6 227 2 AC0944 conserved hypothet
26 47 35.6 341 2 A83644 hypothetical prote
27 47 35.6 413 2 C91229 hypothetical prote
28 47 35.6 413 2 B86076 hypothetical prote
29 47 35.6 418 2 S40824 hypothetical 48K p
30 47 35.6 445 2 A1621 env polyprotein M
31 47 35.6 477 2 S2162 sucrose hydrolase
32 47 35.6 477 2 C91034 sucrose-6 phosphat
33 47 35.6 477 2 D85878 sucrose hydrolase
34 47 35.6 623 2 T47542 Spot 3 protein and
35 47 35.6 628 2 T02602 vacuolar sorting r
36 47 35.6 628 2 T02604 probable vacuolar
37 46.5 35.2 598 2 I51368 gamma-aminobutyric
38 46.5 35.2 794 2 S50657 hypothetical prote
39 46 34.8 221 2 F88082 protein T05A8.2 li
40 46 34.8 262 2 F82519 hypothetical prote
41 46 34.8 469 2 T50934 dioxygenase Dita1,
42 46 34.8 624 2 T00044 vacuolar sorting r
43 46 34.8 625 2 F84706 probable vacuolar
44 46 34.8 643 2 A80787 cytochrome c-type
45 46 34.8 643 2 A80960 cytochrome c-type

Search completed: March 1, 2004, 19:34:28
Job time : 12.5485 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKFRFWTWETWTE 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	40.9	332	2 E69312	nitrate reductase
2	54	40.9	1003	1 GNVWLV	HIV-1 retropepsin
3	54	40.9	1003	1 B44001	HIV-1 retropepsin
4	54	40.9	1003	2 T09440	pol polyprotein -
5	54	40.9	1012	1 GNVWVL	HIV-1 retropepsin
6	54	40.9	1015	1 GNVWH3	HIV-1 retropepsin
7	53	40.2	392	2 G82746	reverse transcript
8	53	40.2	559	2 B47175	hypothetical prote
9	52	39.4	667	1 VCLJGL	env polyprotein pr
10	52	39.4	814	2 A95206	glycoasyl transfera
11	52	39.4	902	2 T01668	pol polyprotein -
12	52	39.4	1002	2 S54378	pol polyprotein -
13	51.5	39.0	1780	2 A85045	probable glucan sy

14 50 37.9 130 2 A82599 conserved hypothet
15 49.5 37.5 148 2 S46315 purindoline-a pre
16 49.5 37.5 222 2 A88102 protein W09G10.1 {
17 48.5 36.7 223 2 A29770 cerebellar degener
18 48.5 36.7 660 2 E81839 probable transmemb
19 48.5 36.7 675 2 E81101 transporter, BCO1
20 48.5 36.7 1103 2 T42022 probable chitin sy
21 48 36.4 1002 1 GN1JND HIV-1 retropepsin
22 47.5 36.0 625 2 T06184 sucrose-fructan 6-
23 47 35.6 86 2 T05982 hypothethical prote
24 47 35.6 198 2 G72489 hypothethical prote
25 47 35.6 227 2 AC0944 conserved hypothet
26 47 35.6 341 2 A83644 hypothethical prote
27 47 35.6 413 2 C91229 hypothethical prote
28 47 35.6 413 2 B86076 hypothethical prote
29 47 35.6 418 2 S40824 hypothethical 48K p
30 47 35.6 445 2 A41621 env polypeptid M
31 47 35.6 477 2 S52162 sucrose hydrolase
32 47 35.6 477 2 C91034 sucrose-6 phosphat
33 47 35.6 477 2 D85878 sucrose hydrolase
34 47 35.6 623 2 T47542 Spot 3 protein and
35 47 35.6 628 2 T02602 vacuolar sorting r
36 47 35.6 628 2 T02604 probable vacuolar
37 46.5 35.2 598 2 I51368 gamma-aminobutyric
38 46.5 35.2 794 2 S06877 hypothethical prote
39 46 34.8 221 2 F88062 protein T05A8.2 (I
40 46 34.8 262 2 F82519 hypothethical prote
41 46 34.8 469 2 T50934 dihydrogenase DitaI,
42 46 34.8 624 2 T00044 vacuolar sorting r
43 46 34.8 625 2 F84706 probable vacuolar
44 46 34.8 643 2 AG0787 cytochrome c-type
45 46 34.8 643 2 AH0960 cytochrome c-type
Search completed: March 1, 2004, 19:34:28
Job time : 12.5485 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.339 Million cell updates/sec

Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 YGFKKFKPTWTWTWTE 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	43.2	1006	1	POL_HV1MN
2	55	41.7	789	1	LP1B_DROME
3	54	40.9	332	1	HMEC_ARCFU
4	54	40.9	1003	1	POL_HV1H2
5	54	40.9	1003	1	POL_HV1Y2
6	54	40.9	1007	1	POL_HV1JR
7	54	40.9	1015	1	POL_HV1B1
8	54	40.9	1015	1	POL_HV1B5
9	54	40.9	1015	1	POL_HV1BR
10	54	40.9	1015	1	POL_HV1PV
11	52	39.4	667	1	ENV_GALV
12	52	39.4	1002	1	POL_HV1EL
13	52	39.4	1002	1	POL_HV1MA
14	52	39.4	1002	1	POL_HV1Z2
15	50	37.5	789	1	LP1A_DROME
16	49.5	37.5	148	1	PUTA_WHEAT
17	49	37.1	856	1	ENV_HV2NZ

P05961 human immun
P11996 drosophila
O29749 archaeglob
P04585 human immun
P35963 human immun
P20875 human immun
P03366 human immun
P04587 human immun
P03367 human immun
P03368 human immun
P21415 gibbon ape
P04589 human immun
P04588 human immun
P12499 human immun
P11995 drosophila
P33432 triticum ae
P05883 human immun

18 49 37.1 1002 1 POL_HV1RH
19 49 37.1 1003 1 POL_HV1NS
20 49 37.1 1003 1 POL_HV1OY
21 48.5 36.7 223 1 CDRI_HUMAN
22 48.5 36.7 1103 1 CHS6_USMVA
23 48 36.4 627 1 TES1_MOUSE
24 48 36.4 1002 1 POL_HV1ND
25 47 35.6 227 1 YIIY_SALTY
26 47 35.6 294 1 239F_HUMAN
27 47 35.6 413 1 YIHS_ECOLI
28 47 35.6 477 1 CSCA_ECOLI
29 46.5 35.2 794 1 YB14_YEAST
30 46 34.8 78 1 Y009_BPL2
31 46 34.8 330 1 CATK_PIG
32 46 34.8 859 1 ENV_HV2CA
33 46 34.8 859 1 ENV_HV2D2
34 46 34.8 1002 1 POL_HV1U4
35 46 34.8 1027 1 POL_SIVCZ
36 45.5 34.5 691 1 CQMA_NEIGO
37 45 34.1 132 1 YXEC_BACSU
38 45 34.1 203 1 Y028_MYCPN
39 45 34.1 228 1 IFE2_CABEL
40 45 34.1 329 1 CATK_RABIT
41 45 34.1 344 1 RHAT_ECOLI
42 45 34.1 372 1 SUM1_MOUSE
43 45 34.1 374 1 SUN1_HUMAN
44 45 34.1 377 1 CCHL_SCHPO
45 45 34.1 393 1 DOM3_CABEL

P05959 human immun
P12497 human immun
P20892 human immun
P51861 homo sapien
O13395 ustilago ma
O70146 mus musculu
P18802 human immun
P43022 salmonella
Q15777 homo sapien
P32140 escherichia
P40714 escherichia
P39961 saccharomyc
P42544 bacteriophy
Q9gle3 sus scrofa
P24105 human immun
P15831 human immun
P24740 human immun
P17283 chimpanzee
P51973 neisseria g
P54942 bacillus su
P75083 mycoplasma
Q21693 caenorhabdi
P43236 oryctolagus
P27125 escherichia
Q8r0f3 mus musculu
Q8nbk3 homo sapien
O74794 schizosacch
Q10660 caenorhabdi

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec
Title: US-09-915-914B-5
Perfect score: 132
Sequence: 1 VGFKKFKRWWTWETWTE 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1 60 45.5 560 15 Q90RR5 Q90rr5 human immu
2 60 45.5 560 15 Q90RR6 Q90rr6 human immu
3 60 45.5 560 15 Q90RR4 Q90rr4 human immu
4 58 43.9 1033 15 Q79666 Q79666 human immu
5 57 43.2 225 15 Q988V3 Q988v3 human immu
6 57 43.2 237 15 Q9WGV3 Q9wgv3 human immu
7 57 43.2 237 15 Q9WGV7 Q9wgv7 human immu
8 57 43.2 237 15 Q9WGV5 Q9wgv5 human immu
9 57 43.2 237 15 Q9WGV0 Q9wgv0 human immu
10 57 43.2 237 15 Q9WGV5 Q9wgv5 human immu
11 57 43.2 237 15 Q9WGV9 Q9wgv9 human immu
12 57 43.2 237 15 Q9WGH5 Q9wgh5 human immu
13 57 43.2 237 15 Q9WGX6 Q9wgx6 human immu
14 57 43.2 237 15 Q9WGX2 Q9wgx2 human immu
15 57 43.2 237 15 Q9WGX5 Q9wgx5 human immu
16 57 43.2 237 15 Q9WGW6 Q9wgv6 human immu
17 57 43.2 237 15 Q9WGV6 Q9wgv6 human immu
18 57 43.2 237 15 Q9WGV8 Q9wgv8 human immu
19 57 43.2 237 15 Q9WGV3 Q9wgv3 human immu
20 57 43.2 237 15 Q9WGW4 Q9wgv4 human immu
21 57 43.2 237 15 Q9WGV4 Q9wgv4 human immu
22 57 43.2 519 15 Q9ID13 Q9id13 human immu
23 57 43.2 523 15 Q9ID19 Q9id19 human immu
24 57 43.2 523 15 Q9IDC7 Q9idc7 human immu
25 57 43.2 523 15 Q9IDF2 Q9idf2 human immu
26 57 43.2 524 15 Q9IDF8 Q9idf8 human immu
27 57 43.2 524 15 Q9ID17 Q9id17 human immu
28 57 43.2 524 15 Q9ID18 Q9id18 human immu
29 57 43.2 524 15 Q9IDB9 Q9idb9 human immu
30 57 43.2 524 15 Q9IDD1 Q9idd1 human immu
31 57 43.2 524 15 Q9ID16 Q9id16 human immu
32 57 43.2 524 15 Q9IDF8 Q9idf8 human immu
33 57 43.2 524 15 Q9ID12 Q9id12 human immu
34 57 43.2 524 15 Q9ID14 Q9id14 human immu
35 57 43.2 524 15 Q9ID15 Q9id15 human immu
36 57 43.2 524 15 Q9IDD2 Q9idd2 human immu
37 57 43.2 547 15 Q90S79 Q90s79 human immu
38 57 43.2 547 15 Q90S76 Q90s76 human immu
39 57 43.2 547 15 Q90S80 Q90s80 human immu
40 57 43.2 547 15 Q90S77 Q90s77 human immu
41 57 43.2 547 15 Q90S81 Q90s81 human immu
42 57 43.2 560 15 Q90S78 Q90s78 human immu
43 57 43.2 560 15 Q90RS2 Q90rs2 human immu
44 57 43.2 560 15 Q90RP0 Q90rp0 human immu
45 57 43.2 560 15 Q99BA6 Q99ba6 human immu
Q71157 human immu

Search completed: March 1, 2004, 19:31:52
Job time : 35.5802 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 13:31:13 ; Search time 50.3679 Seconds
(without alignments)
106.584 Million cell updates/sec

Title: US-09-915-914B-6

Perfect score: 119

Sequence: 1 KKKRKVKETWETWETV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
1	119	100.0	19	5	ABB77670	ABB77670	Peptide t
2	74	62.2	20	5	ABB77694	Abb77694	Peptide t
3	74	62.2	21	5	ABB77674	Abb77674	Peptide t
4	70	58.8	19	5	ABB10106	Abb10106	Peptide t
5	70	58.8	19	5	ABB77699	Abb77699	Peptide t
6	69	58.0	19	5	ABB77668	Abb77668	Peptide t
7	69	58.0	19	5	ABB77698	Abb77698	Peptide t
8	69	58.0	19	5	ABB77669	Abb77669	Peptide t
9	68	57.1	20	5	ABB77679	Abb77679	Generic p

10 66.5 55.9 17 5 ABB77667
11 64.5 54.2 18 5 ABB77666
12 64 53.8 11 5 ABB77695
13 64 53.8 12 5 ABB77699
14 64 53.8 12 5 ABB56174
15 64 53.8 13 5 ABB77676
16 64 53.8 20 5 ABB77672
17 64 53.8 20 5 ABB77673
18 64 53.8 21 5 ABB78995
19 64 53.8 21 5 ABB77693
20 64 53.8 21 5 ABB77671
21 64 53.8 21 7 ABB68484
22 64 53.8 21 7 ADC22460
23 64 53.8 26 5 ABB58200
24 61 51.3 21 5 ABB77665
25 59 49.6 9 5 ABB77692
26 57 47.9 418 3 ABB35809
27 57 47.9 496 4 ABB25893
28 57 47.9 928 4 ABB30068
29 57 47.9 928 4 ABB25926
30 55 46.2 1510 5 ABB91970
31 55 46.2 1662 5 ABB93630
32 55 46.2 1858 5 ABB90859
33 54 45.4 21 5 ABB77678
34 53.5 45.0 19 5 ABB77675
35 52 43.7 265 4 ABB80417
36 52 43.7 286 4 ABB54774
37 52 43.7 383 3 ABB42073
38 52 43.7 432 3 ABB42072
39 52 43.7 435 3 ABB42071
40 52 43.7 784 5 ABB92019
41 52 43.7 1346 3 ABB39112
42 52 43.7 1390 3 ABB39111
43 52 43.7 1403 3 ABB39110
44 51 42.9 24 4 ABB60395
45 51 42.9 24 4 ABB54745

ALIGNMENTS

RESULT 1
ID ABB77670 standard; peptide; 19 AA.
XX
AC ABB77670;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.7.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.

XX PD 07-FEB-2002.
XX
XX 26-JUL-2001; 2001WO-US023406.
XX PF
XX 31-JUL-2000; 2000US-0221932P.
XX PR
XX (ACTI-) ACTIVE NOTIF.
XX PA (CNRS) CENT NAT RECH SCI.
XX PA Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
XX PI Horndorp K;
XX PI
XX WPI; 2002-329441/36.
XX
XX Transfection agent that comprises a peptide comprising hydrophobic and
XX hydrophilic domain and having amino acid residues of specified length is
XX useful for a non-covalent association with and transport of a
XX heterologous compound into a cell.
XX
XX Claim 12; Page 16; 156pp; English.
XX
XX The invention relates to a transfection agent comprising a peptide of
XX about 16 - 30 amino acids in length. Peptides of the invention comprise a
XX hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
XX between the domains and a functional group conjugated to at least one
XX terminal of the peptide. Peptides of the invention are useful for a non-
XX covalent association with and transport of a heterologous compound into a
XX cell. They are also useful for promoting the cellular internalisation of
XX at least one member e.g. peptide, proteins, antibodies, their derivatives
XX and/or conjugates. They may form part of a pharmaceutical composition to
XX deliver the compound selected from a diagnostic or therapeutic compound,
XX to treat at least one condition such as cancer or an infectious disease,
XX or which targets a cancerous cell or pathogen-infected cell and to
XX deliver a peptide or inhibitor that disrupts the activity of the enzyme.
XX The agent of the invention has a transfection efficiency of at least 5%
XX for at least two of the members of the group of the compounds. The agent
XX has a good delivery efficiency for a broad spectrum of compounds and cell
XX types, has a low toxicity, are easy to handle and easy to formulate in
XX conjunction with the many different compound types that it can deliver.
XX The peptides are serum sensitive, thus they bode particularly well for
XX systemic and/or localised in patients. The current sequence represents
XX the peptide transfection agent Pep-2.7
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 119; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKKRKYKPEWTWETWETV 19
Db 1 KKKRKYKPEWTWETWETV 19
Search completed: March 1, 2004, 16:55:55
Job time : 53.3679 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:46:26 ; Search time 12.4575 Seconds
(without alignments)
146.709 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKKRKYKPEIWTWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues 283366
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78: +
1: pir1: +
2: pir2: +
3: pir3: +
4: pir4: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	47.9	418	2 S40824	hypothetical 48k p
2	55	46.2	352	2 G84352	general stress pro
3	55	46.2	1510	2 C84727	probable glucan sy
4	55	46.2	1878	2 E86189	hypothetical prote
5	54	45.4	413	2 C91229	hypothetical prote
6	54	45.4	413	2 B86076	hypothetical prote
7	52	43.7	784	2 E84785	probable glucan sy
8	51	42.9	390	1 A60424	calsequestrin prec
9	51	42.9	395	1 A23887	beta-galactosidase
10	51	42.9	1036	2 T05687	hypothetical prote
11	50.5	42.4	571	2 C90391	HIV-1 retropepsin
12	49.5	41.6	1002	1 GNLJND	HIV-1 retropepsin
13	49.5	41.6	1003	1 GNVWLV	HIV-1 retropepsin

14	49.5	41.6	1003	1	B44001	HIV-1 retropepsin
15	49.5	41.6	1003	2	T09440	pol polyprotein -
16	49.5	41.6	1012	1	GNVWLV	HIV-1 retropepsin
17	49.5	41.6	1015	1	GNVWH3	HIV-1 retropepsin
18	49	41.2	683	2	T00872	probable protein k
19	48.5	40.8	766	2	S37894	hypothetical prote
20	48	40.3	197	2	S53053	hypothetical prote
21	48	40.3	314	2	T32293	hypothetical prote
22	48	40.3	797	2	JC4078	protective surface
23	48	40.3	808	2	F64102	protective surface
24	47.5	39.9	463	2	T48116	hypothetical prote
25	47.5	39.9	559	2	B47175	reverse transcript
26	47	39.5	247	2	T37820	hypothetical prote
27	47	39.5	292	2	T30321	hypothetical prote
28	47	39.5	322	1	HLHUR2	T-cell surface gly
29	47	39.5	1963	2	T49914	callose synthase c
30	47	39.5	2831	2	T31419	cyclic beta 1-2 gl
31	47	39.5	2867	2	AG3481	cellobiose-phospho
32	46.5	39.1	1002	2	S54378	pol polyprotein -
33	46	38.7	119	2	D84845	hypothetical prote
34	46	38.7	331	2	A61046	ecdysone-induced m
35	46	38.7	510	2	D70480	acetyl-coenzyme A
36	46	38.7	513	2	E72495	probable acetyl-co
37	46	38.7	524	2	AB2338	acetyl-coenzyme A
38	46	38.7	558	2	G69126	acetyl-CoA synthet
39	46	38.7	645	2	A83054	acetyl-coenzyme A
40	46	38.7	646	2	C86441	probable ABC trans
41	46	38.7	647	2	C87693	acetyl-CoA synthet
42	46	38.7	647	2	E82579	acetyl coenzyme A
43	46	38.7	649	2	D75270	acetyl-CoA synthas
44	46	38.7	651	2	D70769	probable acetyl-co
45	46	38.7	651	2	D83534	acetyl-coenzyme A

Search completed: March 1, 2004, 19:34:30
Job time : 14.5485 secs

OM protein - protein search, using sw model

Run on: March 1, 2004, 16:39:39 ; Search time 7.70755 Seconds
(without alignments)
128.359 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKKRKYPETWETWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	57	47.9	413	1	YIHS_ECOLI	P32140 escherichia
2	51	42.9	390	1	CA01_HUMAN	P31415 homo sapien
3	51	42.9	395	1	CA01_RABIT	P07221 oryctolagus
4	51	42.9	399	1	CA01_MOUSE	O09165 mus musculu
5	49.5	41.6	504	1	YC03_KLEFN	Q46449 klebsiella
6	49.5	41.6	1002	1	POL_HVIND	P18802 human immun
7	49.5	41.6	1003	1	POL_HV1H2	P04585 human immun
8	49.5	41.6	1003	1	POL_HV1V2	P35963 human immun
9	49.5	41.6	1007	1	POL_HV1JUR	P20875 human immun
10	49.5	41.6	1015	1	POL_HV1B1	P03366 human immun
11	49.5	41.6	1015	1	POL_HV1B5	P03367 human immun
12	49.5	41.6	1015	1	POL_HV1BR	P03368 human immun
13	49.5	41.6	1015	1	POL_HV1PV	P36085 saccharomyc
14	48.5	40.8	766	1	STB6_YEAST	O32629 haemophilus
15	48	40.3	793	1	D153_HAEIN	P44935 haemophilus
16	48	40.3	795	1	D152_HAEIN	P46024 haemophilus
17	48	40.3	797	1	D151_HAEIN	

18	47	39.5	51	1	Y04J_BPT4	P39490 bacterioph
19	47	39.5	247	1	YE95_SCHPO	O13767 schizosach
20	47	39.5	322	1	CD1E_HUMAN	P15812 homo sapien
21	46.5	39.1	1002	1	POL_HV1EL	P04589 human immun
22	46.5	39.1	1002	1	POL_HV1Z2	P12499 human immun
23	46.5	39.1	1006	1	POL_HV1MN	P05961 human immun
24	46	38.7	641	1	ACSA_PRB01	Q9F715 gamma-prote
25	46	38.7	644	1	ACSA_PSEPK	O88dw6 pseudomonas
26	46	38.7	645	1	ACSA_PSEAE	Q9hv66 pseudomonas
27	46	38.7	647	1	ACSA_CAUCR	Q9a210 caulobacter
28	46	38.7	647	1	ACSA_XANAC	Q8pf09 xanthomonas
29	46	38.7	647	1	ACSA_XANCP	Q8p311 xanthomonas
30	46	38.7	647	1	ACSA_XYLFA	Q9pb89 xylella fas
31	46	38.7	647	1	ACSA_XYLFT	O87c00 xylella fas
32	46	38.7	648	1	ACSA_BRAJA	Q89wv5 bradyrhizob
33	46	38.7	649	1	ACS2_RHIME	Q92kx2 rhizobium m
34	46	38.7	649	1	ACSA_DEIRA	Q9rl17 deinococcus
35	46	38.7	649	1	ACSA_VIBCH	Q9kv59 vibrio chol
36	46	38.7	650	1	ACSA_SHEON	Q8edk3 shewanella
37	46	38.7	650	1	ACSA_VIBPA	O87ku7 vibrio para
38	46	38.7	650	1	ACSA_VIBVU	O8dcz9 vibrio vuln
39	46	38.7	651	1	ACSL_PSEAE	Q91558 pseudomonas
40	46	38.7	651	1	ACSA_AGRU5	O8ubv5 agrobacteri
41	46	38.7	651	1	ACSA_BRUME	O8vj48 bruceella me
42	46	38.7	651	1	ACSA_BRUSU	Q8fyq3 bruceella su
43	46	38.7	651	1	ACSA_MYCBO	P59871 mycobacteri
44	46	38.7	651	1	ACSA_MYCTU	O69635 mycobacteri
45	46	38.7	651	1	ACSA_PSESM	Q885k7 pseudomonas

Search completed: March 1, 2004, 19:25:02
Job time : 7.70755 secs

OM protein - protein search, using sw model
Run on: March 1, 2004, 16:40:39 ; Search time 35.5802 Seconds
(without alignments)
168.488 Million cell updates/sec

Title: US-09-915-914B-6
Perfect score: 119
Sequence: 1 KKKRKYPERWETWETV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_25:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_rhnc:.*
8: sp_organelle:.*
9: sp_phage:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_rvirus:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	58	48.7	793	17	Q8TVU1	Q8tvul methanopyru
2	57	47.9	413	16	Q7UB71	Q7ub71 shigella fl
3	57	47.9	418	16	Q83IV0	Q83iv0 shigella fl
4	55	46.2	193	16	Q8ETU3	Q8etu3 lactobacill
5	55	46.2	352	17	Q9HNN3	Q9hnn3 halobacteri
6	55	46.2	735	10	Q8GYW2	Q8gyw2 arabidopsis
7	55	46.2	901	10	Q9LRA3	Q9lra3 arabidopsis
8	55	46.2	908	10	Q7XJC6	Q7xjc6 oryza sativ
9	55	46.2	1341	10	Q91TGS	Q91tgs arabidopsis
10	55	46.2	1510	10	Q9SL03	Q9sl03 arabidopsis
11	55	46.2	1878	10	Q9SYJ7	Q9syj7 arabidopsis
12	55	46.2	1950	10	Q9AUE0	Q9aue0 arabidopsis
13	54	45.4	66	5	Q9BPC0	Q9bpc0 conus tessu
14	54	45.4	413	16	Q8XBD6	Q8xbd6 escherichia
15	53	44.5	427	9	Q36164	Q36164 actinophaga
16	53	44.5	1642	10	Q8S5U9	Q8s5u9 cryza sativ
17	53	44.5	3070	12	Q89906	Q89906 sugar beet
18	53	44.5	3074	12	Q08534	Q08534 sugar beet
19	53	44.5	3090	12	Q9Q703	Q9q703 sugar beet
20	52	43.7	79	5	Q9BFC5	Q9bpc5 conus ventr
21	52	43.7	322	10	Q9SHN5	Q9shn5 arabidopsis
22	52	43.7	392	16	Q82GV6	Q82gv6 streptomyce
23	52	43.7	784	10	Q9SJM0	Q9sjm0 arabidopsis
24	51.5	43.3	587	15	Q8Q879	Q8q879 human immun
25	51	42.9	102	6	Q8MIA4	Q8mia4 sus scrofa
26	51	42.9	1036	10	Q9SZN8	Q9szn8 arabidopsis
27	51	42.9	2120	5	Q8IAK1	Q8iak1 plasmodium
28	50.5	42.4	524	15	Q9IDJ7	Q9idj7 human immun
29	50.5	42.4	571	17	Q97WK0	Q97wk0 sulfolobus
30	50.5	42.4	1009	15	Q8JAX3	Q8jax3 human immun
31	50	42.0	74	5	Q9BPC9	Q9bpc9 conus ventr
32	50	42.0	648	5	Q961F2	Q961f2 drosophila
33	50	42.0	970	5	Q9VNZ8	Q9vnz8 drosophila
34	50	42.0	1745	10	Q9LWU7	Q9lww7 oryza sativ
35	49.5	41.6	95	5	Q8MVV0	Q8mvv0 plasmodium
36	49.5	41.6	212	15	Q9WGU7	Q9wgu7 human immun
37	49.5	41.6	237	15	Q9WGV0	Q9wgv0 human immun
38	49.5	41.6	237	15	Q9WGY5	Q9wgy5 human immun
39	49.5	41.6	237	15	Q9WGX9	Q9wgx9 human immun
40	49.5	41.6	237	15	Q9WGT7	Q9wgy7 human immun
41	49.5	41.6	237	15	Q9WGY3	Q9wgy3 human immun
42	49.5	41.6	237	15	Q9W9U0	Q9w9u0 human immun
43	49.5	41.6	237	15	Q9WGY1	Q9wgy1 human immun
44	49.5	41.6	237	15	Q9WGV2	Q9wgv2 human immun
45	49.5	41.6	237	15	Q9WGU8	Q9wgu8 human immun

Search completed: March 1, 2004, 19:31:58
Job time : 41.5802 secs